



SEQUENCE LISTING

<110> NPS PHARMACEUTICALS, INC.
STORMANN, Thomas

<120> G-PROTEIN FUSION RECEPTORS AND CHIMERIC GABAB RECEPTORS

<130> 072827-1801

<140> US 09/679,664

<141> 2000-10-03

<150> US 60/080,671

<151> 1998-04-03

<150> PCT/US99/07333

<151> 1999-04-02

<160> 57

<170> PatentIn version 3.0

<210> 1

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<212> PRT

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<221> misc_feature

<223> CaR extracellular domain

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Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
20 25 30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
35 40 45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
50 55 60

Phe	Arg	Gly	Phe	Arg	Trp	Leu	Gln	Ala	Met	Ile	Phe	Ala	Ile	Glu	Glu	65	70	75	80
Ile	Asn	Ser	Ser	Pro	Ala	Leu	Leu	Pro	Asn	Leu	Thr	Leu	Gly	Tyr	Arg	85	90	95	
Ile	Phe	Asp	Thr	Cys	Asn	Thr	Val	Ser	Lys	Ala	Leu	Glu	Ala	Thr	Leu	100	105	110	
Ser	Phe	Val	Ala	Gln	Asn	Lys	Ile	Asp	Ser	Leu	Asn	Leu	Asp	Glu	Phe	115	120	125	
Cys	Asn	Cys	Ser	Glu	His	Ile	Pro	Ser	Thr	Ile	Ala	Val	Val	Gly	Ala	130	135	140	
Thr	Gly	Ser	Gly	Val	Ser	Thr	Ala	Val	Ala	Asn	Leu	Leu	Gly	Leu	Phe	145	150	155	160
Tyr	Ile	Pro	Gln	Val	Ser	Tyr	Ala	Ser	Ser	Ser	Arg	Leu	Leu	Ser	Asn	165	170	175	
Lys	Asn	Gln	Phe	Lys	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp	Glu	His	180	185	190	
Gln	Ala	Thr	Ala	Met	Ala	Asp	Ile	Ile	Glu	Tyr	Phe	Arg	Trp	Asn	Trp	195	200	205	
Val	Gly	Thr	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Arg	Pro	Gly	Ile	Glu	210	215	220	
Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	Ile	Asp	Phe	Ser	225	230	235	240
Glu	Leu	Ile	Ser	Gln	Tyr	Ser	Asp	Glu	Glu	Glu	Ile	Gln	His	Val	Val	245	250	255	
Glu	Val	Ile	Gln	Asn	Ser	Thr	Ala	Lys	Val	Ile	Val	Val	Phe	Ser	Ser	260	265	270	
Gly	Pro	Asp	Leu	Glu	Pro	Leu	Ile	Lys	Glu	Ile	Val	Arg	Arg	Asn	Ile	275	280	285	
Thr	Gly	Lys	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp	Ala	Ser	Ser	Ser	Leu	290	295	300	
Ile	Ala	Met	Pro	Gln	Tyr	Phe	His	Val	Val	Gly	Gly	Thr	Ile	Gly	Phe	305	310	315	320

Ala	Leu	Lys	Ala	Gly	Gln	Ile	Pro	Gly	Phe	Arg	Glu	Phe	Leu	Lys	Lys	
				325					330					335		
Val	His	Pro	Arg	Lys	Ser	Val	His	Asn	Gly	Phe	Ala	Lys	Glu	Phe	Trp	
			340					345					350			
Glu	Glu	Thr	Phe	Asn	Cys	His	Leu	Gln	Glu	Gly	Ala	Lys	Gly	Pro	Leu	
		355					360					365				
Pro	Val	Asp	Thr	Phe	Leu	Arg	Gly	His	Glu	Glu	Ser	Gly	Asp	Arg	Phe	
	370					375					380					
Ser	Asn	Ser	Ser	Thr	Ala	Phe	Arg	Pro	Leu	Cys	Thr	Gly	Asp	Glu	Asn	
385					390					395					400	
Ile	Ser	Ser	Val	Glu	Thr	Pro	Tyr	Ile	Asp	Tyr	Thr	His	Leu	Arg	Ile	
				405					410					415		
Ser	Tyr	Asn	Val	Tyr	Leu	Ala	Val	Tyr	Ser	Ile	Ala	His	Ala	Leu	Gln	
			420					425					430			
Asp	Ile	Tyr	Thr	Cys	Leu	Pro	Gly	Arg	Gly	Leu	Phe	Thr	Asn	Gly	Ser	
		435					440					445				
Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp	Gln	Val	Leu	Lys	His	Leu	
	450					455					460					
Arg	His	Leu	Asn	Phe	Thr	Asn	Asn	Met	Gly	Glu	Gln	Val	Thr	Phe	Asp	
465					470					475					480	
Glu	Cys	Gly	Asp	Leu	Val	Gly	Asn	Tyr	Ser	Ile	Ile	Asn	Trp	His	Leu	
				485					490					495		
Ser	Pro	Glu	Asp	Gly	Ser	Ile	Val	Phe	Lys	Glu	Val	Gly	Tyr	Tyr	Asn	
			500					505					510			
Val	Tyr	Ala	Lys	Lys	Gly	Glu	Arg	Leu	Phe	Ile	Asn	Glu	Glu	Lys	Ile	
		515					520					525				
Leu	Trp	Ser	Gly	Phe	Ser	Arg	Glu	Val	Pro	Phe	Ser	Asn	Cys	Ser	Arg	
	530					535					540					
Asp	Cys	Leu	Ala	Gly	Thr	Arg	Lys	Gly	Ile	Ile	Glu	Gly	Glu	Pro	Thr	
545					550					555					560	
Cys	Cys	Phe	Glu	Cys	Val	Glu	Cys	Pro	Asp	Gly	Glu	Tyr	Ser	Asp	Glu	

	565		570		575
Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn					
	580		585		590
Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp					
	595		600		605
Thr Glu Pro Phe					
	610				

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			20					25					30		
Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg															
		35					40					45			
Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu															
	50					55					60				
Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys															
65					70				75					80	
Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys															
				85				90						95	
Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val															
			100					105					110		
Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp															
	115						120					125			

Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	Arg	Ser	Ile
130						135					140				
Cys	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	Gln	Val	Asn
145					150					155					160
Arg	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	Leu	Phe
				165					170					175	
Pro	Met	Ser	Gly	Gly	Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	Pro	Ala	Val
			180					185					190		
Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp
		195					200					205			
Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln
	210					215					220				
Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	Ile	Lys	Ile
225					230					235					240
Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala
				245					250					255	
Ala	Arg	Met	Trp	Asn	Leu	Ile	Val	Leu	Ser	Tyr	Gly	Ser	Ser	Ser	Pro
			260					265					270		
Ala	Leu	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro
		275					280					285			
Ser	Ala	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp
	290					295					300				
Gly	Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr
305					310					315					320
Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu
				325					330					335	
Ile	Thr	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys
			340					345					350		
Asn	Leu	Lys	Arg	Gln	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu
		355					360					365			
Thr	Glu	Ala	Arg	Lys	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe

370						375						380					
Gly	Lys	Lys	Tyr	Val	Trp	Phe	Leu	Ile	Gly	Trp	Ile	Ala	Asp	Asn	Trp		
385					390					395					400		
Phe	Lys	Ile	Tyr	Asp	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	Glu	Met	Thr		
				405					410					415			
Glu	Ala	Val	Glu	Gly	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro		
			420					425					430				
Ala	Asn	Thr	Arg	Ser	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu		
		435					440					445					
Lys	Leu	Thr	Lys	Arg	Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	Gly	Gly	Phe		
	450					455					460						
Gln	Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala		
465					470					475						480	
Leu	Asn	Lys	Thr	Ser	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu		
				485					490					495			
Asp	Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala		
			500					505					510				
Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp		
		515					520					525					
Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly		
	530					535					540						
Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu		
545					550					555					560		
Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp		
				565					570					575			
Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys				
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 <223> GABA-betaR1b extracellular domain

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Pro	His	Leu	Pro	Arg	Pro	His	Ser	Arg	Val	Pro	Pro	His	Pro	Ser	Ser	35	40	45	
Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	Leu	Phe	Pro	Met	Ser	Gly	Gly	50	55	60	
Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	Pro	Ala	Val	Glu	Met	Ala	Leu	Glu	65	70	75	80
Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp	Tyr	Glu	Leu	Lys	Leu	85	90	95	
Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln	Ala	Thr	Lys	Tyr	Leu	100	105	110	
Tyr	Glu	Leu	Leu	Asn	Tyr	Asp	Pro	Ile	Lys	Ile	Ile	Leu	Met	Pro	Gly	115	120	125	
Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala	Ala	Arg	Met	Trp	Asn	130	135	140	
Leu	Ile	Val	Leu	Ser	Tyr	Gly	Ser	Ser	Ser	Pro	Ala	Leu	Ser	Asn	Arg	145	150	155	160
Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	Ser	Ala	Thr	Leu	His	165	170	175	
Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	Gly	Trp	Lys	Lys	Ile	180	185	190	

Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	Ser	Thr	Leu	Asp	Asp	195	200	205
Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	Ile	Thr	Phe	Arg	Gln	210	215	220
Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn	Leu	Lys	Arg	Gln	225	230	235
Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	Thr	Glu	Ala	Arg	Lys	245	250	255
Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe	Gly	Lys	Lys	Tyr	Val	260	265	270
Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	Asn	Trp	Phe	Lys	Ile	Tyr	Asp	275	280	285
Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	Glu	Met	Thr	Glu	Ala	Val	Glu	Gly	290	295	300
His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser	305	310	315
Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg	325	330	335
Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	Gly	Gly	Phe	Gln	Glu	Ala	Pro	Leu	340	345	350
Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala	Leu	Asn	Lys	Thr	Ser	355	360	365
Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	370	375	380
Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser	385	390	395
Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	405	410	415
Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	420	425	430
Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr			

435 440 445
 Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile
 450 455 460

 Lys Thr Phe Arg Phe Leu Ser Gln Lys
 465 470

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 <223> Xaa is any amino acid

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 <223> GABA-betaR2 extracellular domain

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 Leu Pro Leu Ala Pro Gly Ala Trp Gly Trp Ala Arg Gly Ala Pro Arg
 35 40 45

 Pro Pro Pro Ser Ser Pro Pro Leu Ser Ile Met Gly Leu Met Pro Leu
 50 55 60

 Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg Gly Val Leu Pro Ala
 65 70 75 80

 Val Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu Ser Leu Leu Arg Pro
 85 90 95

 Tyr Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu Cys Asp Asn Ala Lys
 100 105 110

 Gly Leu Lys Ala Phe Tyr Asp Ala Ile Lys Tyr Gly Pro Asn His Leu

115					120					125					
Met	Val	Phe	Gly	Gly	Val	Cys	Pro	Ser	Val	Thr	Ser	Ile	Ile	Ala	Glu
130						135					140				
Ser	Leu	Gln	Gly	Trp	Asn	Leu	Val	Gln	Leu	Ser	Phe	Ala	Ala	Thr	Thr
145					150					155					160
Pro	Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Phe	Phe	Arg	Thr	Val
				165					170					175	
Pro	Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu	Lys	Leu	Leu	Lys	His
			180					185					190		
Tyr	Gln	Trp	Lys	Arg	Val	Gly	Thr	Leu	Thr	Gln	Asp	Val	Gln	Arg	Phe
	195						200					205			
Ser	Glu	Val	Arg	Asn	Asp	Leu	Thr	Gly	Val	Leu	Tyr	Gly	Glu	Asp	Ile
	210					215					220				
Glu	Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp	Pro	Cys	Thr	Ser	Val
225					230					235					240
Lys	Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile	Leu	Gly	Gln	Phe	Asp
				245					250					255	
Gln	Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala	Tyr	Glu	Glu	Asn	Met
			260					265					270		
Tyr	Gly	Ser	Lys	Tyr	Gln	Trp	Ile	Ile	Pro	Gly	Trp	Tyr	Glu	Pro	Ser
		275					280					285			
Trp	Trp	Glu	Gln	Val	His	Thr	Glu	Ala	Asn	Ser	Ser	Arg	Cys	Leu	Arg
	290					295					300				
Lys	Asn	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile	Gly	Val	Asp	Phe	Glu
305					310					315					320
Pro	Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser	Gly	Lys	Thr	Pro	Gln
				325					330					335	
Gln	Tyr	Glu	Arg	Glu	Tyr	Asn	Asn	Lys	Arg	Ser	Gly	Val	Gly	Pro	Ser
			340					345					350		
Lys	Phe	His	Gly	Tyr	Ala	Tyr	Asp	Gly	Ile	Trp	Val	Ile	Ala	Lys	Thr
		355					360					365			

Leu Gln Arg Ala Met Glu Thr Leu His Ala Ser Ser Arg His Gln Arg
 370 375 380
 Ile Gln Asp Phe Asn Tyr Thr Asp His Thr Leu Gly Arg Ile Ile Leu
 385 390 395 400
 Asn Ala Met Asn Glu Thr Asn Phe Phe Gly Val Thr Gly Gln Val Val
 405 410 415
 Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln
 420 425 430
 Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr
 435 440 445
 Leu Glu Ile Ile Asn Asp Thr Ile Arg Phe Gln Gly Ser Glu Pro Pro
 450 455 460
 Lys Asp Lys Thr Ile Ile Leu Glu Gln Leu Arg Lys Ile Ser Leu Pro
 465 470 475 480

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 <223> mGluR8 extracellular domain

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 Ser Gln Glu Tyr Ala His Ser Ile Arg Val Asp Gly Asp Ile Ile Leu
 35 40 45
 Gly Gly Leu Phe Pro Val His Ala Lys Gly Glu Arg Gly Val Pro Cys
 50 55 60
 Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu

65					70					75				80
Tyr	Ala	Ile	Asp	Gln	Ile	Asn	Lys	Asp	Pro	Asp	Leu	Leu	Ser	Asn Ile
				85					90					95
Thr	Leu	Gly	Val	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr Ala
			100					105					110	
Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Glu	Lys	Asp Ala
		115					120					125		
Ser	Asp	Val	Lys	Cys	Ala	Asn	Gly	Asp	Pro	Pro	Ile	Phe	Thr	Lys Pro
	130					135					140			
Asp	Lys	Ile	Ser	Gly	Val	Ile	Gly	Ala	Ala	Ala	Ser	Ser	Val	Ser Ile
145					150					155				160
Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser Tyr
			165						170					175
Ala	Ser	Thr	Ala	Pro	Glu	Leu	Ser	Asp	Asn	Thr	Arg	Tyr	Asp	Phe Phe
			180					185					190	
Ser	Arg	Val	Val	Pro	Pro	Asp	Ser	Tyr	Gln	Ala	Gln	Ala	Met	Val Asp
		195					200					205		
Ile	Val	Thr	Ala	Leu	Gly	Trp	Asn	Thr	Val	Ser	Thr	Leu	Ala	Ser Glu
	210					215					220			
Gly	Asn	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Thr	Gln	Ile	Ser Arg
225					230					235				240
Glu	Ile	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Gln	Lys	Ile	Pro	Arg Glu
				245					250					255
Pro	Arg	Pro	Gly	Glu	Phe	Glu	Lys	Ile	Ile	Lys	Arg	Leu	Leu	Glu Thr
			260					265					270	
Pro	Asn	Ala	Arg	Ala	Val	Ile	Met	Phe	Ala	Asn	Glu	Asp	Asp	Ile Arg
		275					280					285		
Arg	Ile	Leu	Glu	Ala	Ala	Lys	Lys	Leu	Asn	Gln	Ser	Gly	His	Phe Leu
	290					295					300			
Trp	Ile	Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Tyr Gln
305					310					315				320

Gln	Glu	Glu	Ile	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Ala	
				325					330					335		
Ser	Ile	Asp	Gly	Phe	Asp	Arg	Tyr	Phe	Arg	Ser	Arg	Thr	Leu	Ala	Asn	
			340					345					350			
Asn	Arg	Arg	Asn	Val	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Glu	Asn	Phe	Gly	
			355				360					365				
Cys	Lys	Leu	Gly	Ser	His	Gly	Lys	Arg	Asn	Ser	His	Ile	Lys	Lys	Cys	
	370					375					380					
Thr	Gly	Leu	Glu	Arg	Ile	Ala	Arg	Asp	Ser	Ser	Tyr	Glu	Gln	Glu	Gly	
385					390					395					400	
Lys	Val	Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ser	Met	Ala	Tyr	Ala	Leu	
				405					410					415		
His	Asn	Met	His	Lys	Asp	Leu	Cys	Pro	Gly	Tyr	Ile	Gly	Leu	Cys	Pro	
			420					425					430			
Arg	Met	Ser	Thr	Ile	Asp	Gly	Lys	Glu	Leu	Leu	Gly	Tyr	Ile	Arg	Ala	
			435				440					445				
Val	Asn	Phe	Asn	Gly	Ser	Ala	Gly	Thr	Pro	Val	Thr	Phe	Asn	Glu	Asn	
	450					455					460					
Gly	Asp	Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Phe	Gln	Tyr	Gln	Ile	Thr	Asn	
465					470					475					480	
Lys	Ser	Thr	Glu	Tyr	Lys	Val	Ile	Gly	His	Trp	Thr	Asn	Gln	Leu	His	
				485					490					495		
Leu	Lys	Val	Glu	Asp	Met	Gln	Trp	Ala	His	Arg	Glu	His	Thr	His	Pro	
			500					505					510			
Ala	Ser	Val	Cys	Ser	Leu	Pro	Cys	Lys	Pro	Gly	Glu	Arg	Lys	Lys	Thr	
			515				520					525				
Val	Lys	Gly	Val	Pro	Cys	Cys	Trp	His	Cys	Glu	Arg	Cys	Glu	Gly	Tyr	
	530					535					540					
Asn	Tyr	Gln	Val	Asp	Glu	Leu	Ser	Cys	Glu	Leu	Cys	Pro	Leu	Asp	Gln	
545					550					555					560	
Arg	Pro	Asn	Met	Asn	Arg	Thr	Gly	Cys	Gln	Leu	Ile	Pro	Ile	Ile	Lys	
				565					570					575		

Leu Glu Trp His Ser Pro Trp
580

<210> 6
<211> 250
<212> PRT
<213> Human

<220>
<221> misc_feature
<223> CaR transmembrane domain

<400> 6

Gly	Ile	Ala	Leu	Thr	Leu	Phe	Ala	Val	Leu	Gly	Ile	Phe	Leu	Thr	Ala
1				5					10					15	
Phe	Val	Leu	Gly	Val	Phe	Ile	Lys	Phe	Arg	Asn	Thr	Pro	Ile	Val	Lys
		20					25						30		
Ala	Thr	Asn	Arg	Glu	Leu	Ser	Tyr	Leu	Leu	Leu	Phe	Ser	Leu	Leu	Cys
		35					40					45			
Cys	Phe	Ser	Ser	Ser	Leu	Phe	Phe	Ile	Gly	Glu	Pro	Gln	Asp	Trp	Thr
	50					55					60				
Cys	Arg	Leu	Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	Cys	Ile
65					70					75					80
Ser	Cys	Ile	Leu	Val	Lys	Thr	Asn	Arg	Val	Leu	Leu	Val	Phe	Glu	Ala
			85						90					95	
Lys	Ile	Pro	Thr	Ser	Phe	His	Arg	Lys	Trp	Trp	Gly	Leu	Asn	Leu	Gln
			100					105					110		
Phe	Leu	Leu	Val	Phe	Leu	Cys	Thr	Phe	Met	Gln	Ile	Val	Ile	Cys	Val
		115					120					125			
Ile	Trp	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	Gln	Glu	Leu
	130					135					140				
Glu	Asp	Glu	Ile	Ile	Phe	Ile	Thr	Cys	His	Glu	Gly	Ser	Leu	Met	Ala
145					150					155					160

Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe
 165 170 175
 Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala
 180 185 190
 Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser
 195 200 205
 Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser Ala Val
 210 215 220
 Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala Cys Ile
 225 230 235 240
 Phe Phe Asn Lys Ile Tyr Ile Ile Leu Phe
 245 250

<210> 7
 <211> 267
 <212> PRT
 <213> Human

 <220>
 <221> misc_feature
 <223> GABA-betaR1a transmembrane domain

 <400> 7

Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala
 1 5 10 15
 Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile
 20 25 30
 Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser
 35 40 45
 Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile
 50 55 60
 Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
 65 70 75 80
 Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp

85										90					95				
Trp	Val	His	Thr	Val	Phe	Thr	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg				
			100						105					110					
Lys	Thr	Leu	Glu	Pro	Trp	Lys	Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val				
		115					120					125							
Gly	Met	Asp	Val	Leu	Thr	Leu	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu				
	130					135					140								
His	Arg	Thr	Ile	Glu	Thr	Phe	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile				
145					150					155					160				
Asp	Val	Ser	Ile	Leu	Pro	Gln	Leu	Glu	His	Cys	Ser	Ser	Arg	Lys	Met				
			165						170					175					
Asn	Thr	Trp	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu				
			180					185					190						
Leu	Gly	Ile	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys				
		195					200					205							
Ile	Asn	Asp	His	Arg	Ala	Val	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val				
	210					215					220								
Leu	Cys	Leu	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln				
225					230					235					240				
Asp	Ala	Ala	Phe	Ala	Phe	Ala	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr				
			245						250					255					
Ile	Thr	Leu	Val	Val	Leu	Phe	Val	Pro	Lys	Met									
			260					265											

<210> 8
 <211> 267
 <212> PRT
 <213> Human

 <220>
 <221> misc_feature
 <223> GABA-betaR1b transmembrane domain

 <400> 8

Leu	Phe	Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	1	5	10	15
Val	Val	Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	20	25	30	
Gln	Asn	Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	35	40	45	
Leu	Ala	Leu	Ala	Ala	Val	Phe	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	50	55	60	
Gly	Arg	Asn	Gln	Phe	Pro	Phe	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	65	70	75	80
Gly	Leu	Gly	Phe	Ser	Leu	Gly	Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	85	90	95	
Trp	Val	His	Thr	Val	Phe	Thr	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	100	105	110	
Lys	Thr	Leu	Glu	Pro	Trp	Lys	Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val	115	120	125	
Gly	Met	Asp	Val	Leu	Thr	Leu	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	130	135	140	
His	Arg	Thr	Ile	Glu	Thr	Phe	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	145	150	155	160
Asp	Val	Ser	Ile	Leu	Pro	Gln	Leu	Glu	His	Cys	Ser	Ser	Arg	Lys	Met	165	170	175	
Asn	Thr	Trp	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	180	185	190	

Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
 195 200 205

Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
 210 215 220

Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
 225 230 235 240

Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
 245 250 255

Ile Thr Leu Val Val Leu Phe Val Pro Lys Met
 260 265

<210> 9
 <211> 264
 <212> PRT
 <213> Human

<220>
 <221> misc_feature
 <223> GABA-betaR2 transmembrane domain

<400> 9

Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met Ala
 1 5 10 15

Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile
 20 25 30

Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met
 35 40 45

Leu Ser Tyr Ala Ser Ile Phe Leu Phe Gly Leu Asp Gly Ser Phe Val
 50 55 60

Ser Glu Lys Thr Phe Glu Thr Leu Cys Thr Val Arg Thr Trp Ile Leu
 65 70 75 80

Thr Val Gly Tyr Thr Thr Ala Phe Gly Ala Met Phe Ala Lys Thr Trp
 85 90 95

Arg Val His Ala Ile Phe Lys Asn Val Lys Met Lys Lys Lys Ile Ile
 100 105 110
 Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp
 115 120 125
 Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp Pro Leu Arg Arg Thr
 130 135 140
 Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser
 145 150 155 160
 Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr His Met Thr Ile Trp
 165 170 175
 Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu Met Leu Phe Gly Cys
 180 185 190
 Phe Leu Ala Trp Glu Thr Arg Asn Val Ser Ile Pro Ala Leu Asn Asp
 195 200 205
 Ser Lys Tyr Ile Gly Met Ser Val Tyr Asn Val Gly Ile Met Cys Ile
 210 215 220
 Ile Gly Ala Ala Val Ser Phe Leu Thr Arg Asp Gln Pro Asn Val Gln
 225 230 235 240
 Phe Cys Ile Val Ala Leu Val Ile Ile Phe Cys Ser Thr Ile Thr Leu
 245 250 255
 Cys Leu Val Phe Val Pro Lys Leu
 260

<210> 10
 <211> 260
 <212> PRT
 <213> Human

<220>
 <221> misc_feature
 <223> mGluR8 transmembrane domain

<400> 10

Ala Val Val Pro Val Phe Val Ala Ile Leu Gly Ile Ile Ala Thr Thr

1		5		10		15											
Phe	Val	Ile	Val	Thr	Phe	Val	Arg	Tyr	Asn	Asp	Thr	Pro	Ile	Val	Arg		
		20						25					30				
Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	Val	Leu	Leu	Thr	Gly	Ile	Phe	Leu		
		35					40					45					
Cys	Tyr	Ser	Ile	Thr	Phe	Leu	Met	Ile	Ala	Ala	Pro	Asp	Thr	Ile	Ile		
	50					55					60						
Cys	Ser	Phe	Arg	Arg	Val	Phe	Leu	Gly	Leu	Gly	Met	Cys	Phe	Ser	Tyr		
65					70					75					80		
Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg	Ile	His	Arg	Ile	Phe	Glu	Gln		
				85					90					95			
Gly	Lys	Lys	Ser	Val	Thr	Ala	Pro	Lys	Phe	Ile	Ser	Pro	Ala	Ser	Gln		
			100					105					110				
Leu	Val	Ile	Thr	Phe	Ser	Leu	Ile	Ser	Val	Gln	Leu	Leu	Gly	Val	Phe		
		115					120					125					
Val	Trp	Phe	Val	Val	Asp	Pro	Pro	His	Ile	Ile	Ile	Asp	Tyr	Gly	Glu		
	130					135					140						
Gln	Arg	Thr	Leu	Asp	Pro	Glu	Lys	Ala	Arg	Gly	Val	Leu	Lys	Cys	Asp		
145					150					155					160		
Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys	Ser	Leu	Gly	Tyr	Ser	Ile	Leu	Leu		
			165						170					175			
Met	Val	Thr	Cys	Thr	Val	Tyr	Ala	Ile	Lys	Thr	Arg	Gly	Val	Pro	Glu		
			180					185					190				
Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile	Gly	Phe	Thr	Met	Tyr	Thr	Thr	Cys		
		195					200					205					
Ile	Ile	Trp	Leu	Ala	Phe	Ile	Pro	Ile	Phe	Phe	Gly	Thr	Ala	Gln	Ser		
	210					215					220						
Ala	Glu	Lys	Met	Tyr	Ile	Gln	Thr	Thr	Thr	Leu	Thr	Val	Ser	Met	Ser		
225					230					235					240		
Leu	Ser	Ala	Ser	Val	Ser	Leu	Gly	Met	Leu	Tyr	Met	Pro	Lys	Val	Tyr		
				245					250					255			

Ile Ile Ile Phe
260

<210> 11
<211> 216
<212> PRT
<213> Human

<220>
<221> misc_feature
<223> CaR intracellular domain

<400> 11

Lys	Pro	Ser	Arg	Asn	Thr	Ile	Glu	Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	
1				5					10					15		
His	Ala	Phe	Lys	Val	Ala	Ala	Arg	Ala	Thr	Leu	Arg	Arg	Ser	Asn	Val	
			20					25					30			
Ser	Arg	Lys	Arg	Ser	Ser	Ser	Leu	Gly	Gly	Ser	Thr	Gly	Ser	Thr	Pro	
		35					40					45				
Ser	Ser	Ser	Ile	Ser	Ser	Lys	Ser	Asn	Ser	Glu	Asp	Pro	Phe	Pro	Gln	
	50					55					60					
Pro	Glu	Arg	Gln	Lys	Gln	Gln	Gln	Pro	Leu	Ala	Leu	Thr	Gln	Gln	Glu	
65					70					75					80	
Gln	Gln	Gln	Gln	Pro	Leu	Thr	Leu	Pro	Gln	Gln	Gln	Arg	Ser	Gln	Gln	
				85					90					95		
Gln	Pro	Arg	Cys	Lys	Gln	Lys	Val	Ile	Phe	Gly	Ser	Gly	Thr	Val	Thr	
			100					105					110			
Phe	Ser	Leu	Ser	Phe	Asp	Glu	Pro	Gln	Lys	Asn	Ala	Met	Ala	His	Gly	
		115					120					125				
Asn	Ser	Thr	His	Gln	Asn	Ser	Leu	Glu	Ala	Gln	Lys	Ser	Ser	Asp	Thr	
	130					135					140					
Leu	Thr	Arg	His	Gln	Pro	Leu	Leu	Pro	Leu	Gln	Cys	Gly	Glu	Thr	Asp	
145					150					155					160	
Leu	Asp	Leu	Thr	Val	Gln	Glu	Thr	Gly	Leu	Gln	Gly	Pro	Val	Gly	Gly	

	165		170		175										
Asp	Gln	Arg	Pro	Glu	Val	Glu	Asp	Pro	Glu	Glu	Leu	Ser	Pro	Ala	Leu
			180					185					190		
Val	Val	Ser	Ser	Ser	Gln	Ser	Phe	Val	Ile	Ser	Gly	Gly	Gly	Ser	Thr
		195					200					205			
Val	Thr	Glu	Asn	Val	Val	Asn	Ser								
	210					215									

<210> 12
 <211> 104
 <212> PRT
 <213> Human

 <220>
 <221> misc_feature
 <223> GABA-betaR1a intracellular domain

 <400> 12

Arg	Arg	Leu	Ile	Thr	Arg	Gly	Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr
1				5					10					15	
Met	Lys	Thr	Gly	Ser	Ser	Thr	Asn	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg
			20					25					30		
Leu	Leu	Glu	Lys	Glu	Asn	Arg	Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys
		35					40					45			
Glu	Glu	Arg	Val	Ser	Glu	Leu	Arg	His	Gln	Leu	Gln	Ser	Arg	Gln	Gln
	50					55					60				
Leu	Arg	Ser	Arg	Arg	His	Pro	Pro	Thr	Pro	Pro	Glu	Pro	Ser	Gly	Gly
65					70					75				80	
Leu	Pro	Arg	Gly	Pro	Pro	Glu	Pro	Pro	Asp	Arg	Leu	Ser	Cys	Asp	Gly
				85					90					95	
Ser	Arg	Val	His	Leu	Leu	Tyr	Lys								
			100												

<210> 13
 <211> 104
 <212> PRT
 <213> Human

 <220>
 <221> misc_feature
 <223> GABA-betaR1b intracellular domain

 <400> 13

Arg	Arg	Leu	Ile	Thr	Arg	Gly	Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr
1				5					10					15	
Met	Lys	Thr	Gly	Ser	Ser	Thr	Asn	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg
			20					25					30		
Leu	Leu	Glu	Lys	Glu	Asn	Arg	Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys
		35					40					45			
Glu	Glu	Arg	Val	Ser	Glu	Leu	Arg	His	Gln	Leu	Gln	Ser	Arg	Gln	Gln
	50					55				60					
Leu	Arg	Ser	Arg	Arg	His	Pro	Pro	Thr	Pro	Pro	Glu	Pro	Ser	Gly	Gly
65					70					75					80
Leu	Pro	Arg	Gly	Pro	Pro	Glu	Pro	Pro	Asp	Arg	Leu	Ser	Cys	Asp	Gly
				85					90					95	
Ser	Arg	Val	His	Leu	Leu	Tyr	Lys								
				100											

<210> 14
 <211> 197
 <212> PRT
 <213> Human

 <220>
 <221> misc_feature
 <223> GABA-betaR2 intracellular domain

 <400> 14

Ile Thr Leu Arg Thr Asn Pro Asp Ala Ala Thr Gln Asn Arg Arg Phe

1		5		10		15											
Gln	Phe	Thr	Gln	Asn	Gln	Lys	Lys	Glu	Asp	Ser	Lys	Thr	Ser	Thr	Ser		
			20					25					30				
Val	Thr	Ser	Val	Asn	Gln	Ala	Ser	Thr	Ser	Arg	Leu	Glu	Gly	Leu	Gln		
		35					40					45					
Ser	Glu	Asn	His	Arg	Leu	Arg	Met	Lys	Ile	Thr	Glu	Leu	Asp	Lys	Asp		
	50					55					60						
Leu	Glu	Glu	Val	Thr	Met	Gln	Leu	Gln	Asp	Thr	Pro	Glu	Lys	Thr	Thr		
65					70				75						80		
Tyr	Ile	Lys	Gln	Asn	His	Tyr	Gln	Glu	Leu	Asn	Asp	Ile	Leu	Asn	Leu		
				85					90					95			
Gly	Asn	Phe	Thr	Glu	Ser	Thr	Asp	Gly	Gly	Lys	Ala	Ile	Leu	Lys	Asn		
			100					105					110				
His	Leu	Asp	Gln	Asn	Pro	Gln	Leu	Gln	Trp	Asn	Thr	Thr	Glu	Pro	Ser		
		115					120					125					
Arg	Thr	Cys	Lys	Asp	Pro	Ile	Glu	Asp	Ile	Asn	Ser	Pro	Glu	His	Ile		
	130					135					140						
Gln	Arg	Arg	Leu	Ser	Leu	Gln	Leu	Pro	Ile	Leu	His	His	Ala	Tyr	Leu		
145					150					155					160		
Pro	Ser	Ile	Gly	Gly	Val	Asp	Ala	Ser	Cys	Val	Ser	Pro	Cys	Val	Ser		
				165					170					175			
Pro	Thr	Ala	Ser	Pro	Arg	His	Arg	His	Val	Pro	Pro	Ser	Phe	Arg	Val		
			180					185					190				
Met	Val	Ser	Gly	Leu													
				195													

<210> 15
 <211> 65
 <212> PRT
 <213> Human

<220>
 <221> misc_feature
 <223> mGluR8 intracellular domain

<400> 15

His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Phe Lys Ala Val
 1 5 10 15

Val Thr Ala Ala Thr Met Gln Ser Lys Leu Ile Gln Lys Gly Asn Asp
 20 25 30

Arg Pro Asn Gly Glu Val Lys Ser Glu Leu Cys Glu Ser Leu Glu Thr
 35 40 45

Asn Ser Lys Ser Ser Val Glu Phe Pro Met Val Lys Ser Gly Ser Thr
 50 55 60

Ser
 65

<210> 16
 <211> 374
 <212> PRT
 <213> Human

<220>
 <221> misc_feature
 <223> G15 protein

<400> 16

Met Ala Arg Ser Leu Thr Trp Gly Cys Cys Pro Trp Cys Leu Thr Glu
 1 5 10 15

Glu Glu Lys Thr Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu
 20 25 30

Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu

35					40					45					
Gly	Pro	Gly	Glu	Ser	Gly	Lys	Ser	Thr	Phe	Ile	Lys	Gln	Met	Arg	Ile
50					55					60					
Ile	His	Gly	Val	Gly	Tyr	Ser	Glu	Glu	Asp	Arg	Arg	Ala	Phe	Arg	Leu
65				70					75						80
Leu	Ile	Tyr	Gln	Asn	Ile	Phe	Val	Ser	Met	Gln	Ala	Met	Ile	Asp	Ala
			85					90						95	
Met	Asp	Arg	Leu	Gln	Ile	Pro	Phe	Ser	Arg	Pro	Asp	Ser	Lys	Gln	His
			100					105					110		
Ala	Ser	Leu	Val	Met	Thr	Gln	Asp	Pro	Tyr	Lys	Val	Ser	Thr	Phe	Glu
		115					120					125			
Lys	Pro	Tyr	Ala	Val	Ala	Met	Gln	Tyr	Leu	Trp	Arg	Asp	Ala	Gly	Ile
	130					135					140				
Arg	Ala	Cys	Tyr	Glu	Arg	Arg	Arg	Glu	Phe	His	Leu	Leu	Asp	Ser	Ala
145				150						155					160
Val	Tyr	Tyr	Leu	Ser	His	Leu	Glu	Arg	Ile	Ser	Glu	Asp	Ser	Tyr	Ile
			165					170						175	
Pro	Thr	Ala	Gln	Asp	Val	Leu	Arg	Ser	Arg	Met	Pro	Thr	Thr	Gly	Ile
			180					185						190	
Asn	Glu	Tyr	Cys	Phe	Ser	Val	Lys	Lys	Thr	Lys	Leu	Arg	Ile	Val	Asp
		195					200					205			
Val	Gly	Gly	Gln	Arg	Ser	Glu	Arg	Arg	Lys	Trp	Ile	His	Cys	Phe	Glu
	210					215					220				
Asn	Val	Ile	Ala	Leu	Ile	Tyr	Leu	Ala	Ser	Leu	Ser	Glu	Tyr	Asp	Gln
225				230						235					240
Cys	Leu	Glu	Glu	Asn	Asp	Gln	Glu	Asn	Arg	Met	Glu	Glu	Ser	Leu	Ala
				245					250					255	
Leu	Phe	Ser	Thr	Ile	Leu	Glu	Leu	Pro	Trp	Phe	Lys	Ser	Thr	Ser	Val
			260					265					270		
Ile	Leu	Phe	Leu	Asn	Lys	Thr	Asp	Ile	Leu	Glu	Asp	Lys	Ile	His	Thr
		275					280					285			

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp
 290 295 300
 Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr
 305 310 315 320
 Ala Ser Cys Ala Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala
 325 330 335
 Arg Arg Phe Phe Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val
 340 345 350
 Arg Ser Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
 355 360 365
 Asp Glu Ile Asn Leu Leu
 370

<210> 17
 <211> 374
 <212> PRT
 <213> Human

<220>
 <221> misc_feature
 <223> G16 protein

<400> 17

Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
 1 5 10 15
 Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
 20 25 30
 Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Leu
 35 40 45
 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
 50 55 60
 Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
 65 70 75 80
 Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala

85										90					95				
Met	Glu	Arg	Leu	Gln	Ile	Pro	Phe	Ser	Arg	Pro	Glu	Ser	Lys	His	His				
			100					105					110						
Ala	Ser	Leu	Val	Met	Ser	Gln	Asp	Pro	Tyr	Lys	Val	Thr	Thr	Phe	Glu				
		115					120					125							
Lys	Arg	Tyr	Ala	Ala	Ala	Met	Gln	Trp	Leu	Trp	Arg	Asp	Ala	Gly	Ile				
	130					135					140								
Arg	Ala	Cys	Tyr	Glu	Arg	Arg	Arg	Glu	Phe	His	Leu	Leu	Asp	Ser	Ala				
145					150					155					160				
Val	Tyr	Tyr	Leu	Ser	His	Leu	Glu	Arg	Ile	Thr	Glu	Glu	Gly	Tyr	Val				
				165					170					175					
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 <213> Rat

<220>
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 <223> rat GABA-betaR1a

<400> 22

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 <213> Rat

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 <223> rat GABA-betaR1b

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<213> Rat

<220>
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<223> rat GABA-betaR1a

<400> 24

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His	Pro	Pro	Trp	Glu	Gly	Gly	Ile	Arg	Tyr	Arg	Gly	Leu	Thr	Arg	Asp
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Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	Ser	
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Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	Ile	
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Thr	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn		
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Glu	Ala	Arg	Lys	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe	Gly		
	370					375					380						
Lys	Lys	Tyr	Val	Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	Asn	Trp	Phe		
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Lys	Thr	Tyr	Asp	Pro	Ser	Ile	Asn	Cys	Thr	Val	Glu	Glu	Met	Thr	Glu		
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Ala	Val	Glu	Gly	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro	Ala		
			420					425					430				
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		435					440					445					
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	450					455					460						
Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala	Leu		
465					470					475							
Asn	Lys	Thr	Ser	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	Asp		
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Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	Met		
			500					505					510				
Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala		
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Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	Gly		
	530					535					540						
Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	Ser		
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Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp	Gln		
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580					585					590					
Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	Cys
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Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	Ser
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625						630					635				640
Ala	Ala	Val	Phe	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	Gly	Arg	Ser
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Gln	Phe	Pro	Phe	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	Gly	Leu	Gly
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Phe	Ser	Leu	Gly	Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	Trp	Val	His
		675					680					685			
Thr	Val	Phe	Thr	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	Lys	Thr	Leu
	690					695					700				
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705						710					715				720
Val	Leu	Thr	Leu	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	His	Arg	Thr
				725					730					735	
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			740					745					750		
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		755					760					765			
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Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	Thr	Arg	Gly	Glu
	850					855					860				
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865					870					875					880
Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	Glu	Asn	Arg	Glu
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	915						920					925			
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	930					935					940				
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 <213> Rat

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 <223> rat GABA-betaR1b

 <400> 25

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Pro	His	Leu	Pro	Arg	Pro	His	Pro	Arg	Val	Pro	Pro	His	Pro	Ser	Ser
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Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp	Tyr	Glu	Leu	Lys	Leu
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Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln	Ala	Thr	Lys	Tyr	Leu
			100					105					110		
Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	Ile	Lys	Ile	Ile	Leu	Met	Pro	Gly
		115					120					125			
Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala	Ala	Arg	Met	Trp	Asn
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Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn	Leu	Lys	Arg	Gln
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His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser	305	310	315	320
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Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	405	410	415	
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Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	Cys	Leu	Ser	Phe	Asn	485	490	495	
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Ser	Asp	Val	Ser	Ile	Gln	Val	Ala	Asn	Leu	Leu	Arg	Leu	Phe	Gln	Ile		
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Lys	Ala	Met	Ala	Glu	Ile	Leu	Arg	Phe	Phe	Asn	Trp	Thr	Tyr	Val	Ser		
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Trp	Asn	Asn	Ser	Arg	Asn	Pro	Trp	Phe	Arg	Glu	Phe	Trp	Glu	Gln	Arg		
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Phe	Arg	Cys	Ser	Phe	Arg	Gln	Arg	Asp	Cys	Ala	Ala	His	Ser	Leu	Arg	355	360	365
Ala	Val	Pro	Phe	Glu	Gln	Glu	Ser	Lys	Ile	Met	Phe	Val	Val	Asn	Ala	370	375	380
Val	Tyr	Ala	Met	Ala	His	Ala	Leu	His	Asn	Met	His	Arg	Ala	Leu	Cys	385	390	395
Pro	Asn	Thr	Thr	Arg	Leu	Cys	Asp	Ala	Met	Arg	Pro	Val	Asn	Gly	Arg	405	410	415
Arg	Leu	Tyr	Lys	Asp	Phe	Val	Leu	Asn	Val	Lys	Phe	Asp	Ala	Pro	Phe	420	425	430
Arg	Pro	Ala	Asp	Thr	His	Asn	Glu	Val	Arg	Phe	Asp	Arg	Phe	Gly	Asp	435	440	445
Gly	Ile	Gly	Arg	Tyr	Asn	Ile	Phe	Thr	Tyr	Leu	Arg	Ala	Gly	Ser	Gly	450	455	460
Arg	Tyr	Arg	Tyr	Gln	Lys	Val	Gly	Tyr	Trp	Ala	Glu	Gly	Leu	Thr	Leu	465	470	475
Asp	Thr	Ser	Leu	Ile	Pro	Trp	Ala	Ser	Pro	Ser	Ala	Gly	Pro	Leu	Ala	485	490	495
Ala	Ser	Arg	Cys	Ser	Glu	Pro	Cys	Leu	Gln	Asn	Glu	Val	Lys	Ser	Val	500	505	510
Gln	Pro	Gly	Glu	Val	Cys	Cys	Trp	Leu	Cys	Ile	Pro	Cys	Gln	Pro	Tyr	515	520	525
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Leu	Gly	Ala	Leu	Ala	Thr	Leu	Phe	Val	Leu	Gly	Val	Phe	Val	Arg	His	580	585	590
Asn	Ala	Thr	Pro	Val	Val	Lys	Ala	Ser	Gly	Arg	Glu	Leu	Cys	Tyr	Ile	595	600	605

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		675					680					685							
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Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Val	225		230		235
Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg		245		250	255
Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe		260		265	270
Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu		275		280	285
Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala		290		295	300
Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser		305		310	315
Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn		325		330	335
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Ser	Phe	Val	Ala	Gln	Asn	Lys	Ile	Asp	Ser	Leu	Asn	Leu	Asp	Glu	Phe	115	120	125	

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Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp	Gln	Val	Leu	Lys	His	Leu	450	455	460	
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Pro	Val	Asp	Thr	Phe	Leu	Arg	Gly	His	Glu	Glu	Ser	Gly	Asp	Arg	Phe
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Ser	Asn	Ser	Ser	Thr	Ala	Phe	Arg	Pro	Leu	Cys	Thr	Gly	Asp	Glu	Asn	385	390	395	400
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Arg	His	Leu	Asn	Phe	Thr	Asn	Asn	Met	Gly	Glu	Gln	Val	Thr	Phe	Asp	465	470	475	480
Glu	Cys	Gly	Asp	Leu	Val	Gly	Asn	Tyr	Ser	Ile	Ile	Asn	Trp	His	Leu	485	490	495	
Ser	Pro	Glu	Asp	Gly	Ser	Ile	Val	Phe	Lys	Glu	Val	Gly	Tyr	Tyr	Asn	500	505	510	
Val	Tyr	Ala	Lys	Lys	Gly	Glu	Arg	Leu	Phe	Ile	Asn	Glu	Glu	Lys	Ile	515	520	525	
Leu	Trp	Ser	Gly	Phe	Ser	Arg	Glu	Val	Pro	Phe	Ser	Asn	Cys	Ser	Arg	530	535	540	
Asp	Cys	Leu	Ala	Gly	Thr	Arg	Lys	Gly	Ile	Ile	Glu	Gly	Glu	Pro	Thr	545	550	555	560
Cys	Cys	Phe	Glu	Cys	Val	Glu	Cys	Pro	Asp	Gly	Glu	Tyr	Ser	Asp	Glu	565	570	575	
Thr	Asp	Ala	Ser	Ala	Cys	Asn	Lys	Cys	Pro	Asp	Asp	Phe	Trp	Ser	Asn	580	585	590	
Glu	Asn	His	Thr	Ser	Cys	Phe	Glu	Leu	Pro	Gln	Glu	Tyr	Ile	Arg	Trp	595	600	605	
Gly	Asp	Ala	Trp	Ala	Val	Gly	Pro	Val	Thr	Ile	Ala	Cys	Leu	Gly	Ala	610	615	620	
Leu	Ala	Thr	Leu	Phe	Val	Leu	Gly	Val	Phe	Val	Arg	His	Asn	Ala	Thr	625	630	635	640

Pro	Val	Val	Lys	Ala	Ser	Gly	Arg	Glu	Leu	Cys	Tyr	Ile	Leu	Leu	Gly	645	650	655
Gly	Val	Phe	Leu	Cys	Tyr	Cys	Met	Thr	Phe	Ile	Phe	Ile	Ala	Lys	Pro	660	665	670
Ser	Thr	Ala	Val	Cys	Thr	Leu	Arg	Arg	Leu	Gly	Leu	Gly	Thr	Ala	Phe	675	680	685
Ser	Val	Cys	Tyr	Ser	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg	Ile	Ala	Arg	690	695	700
Ile	Phe	Gly	Gly	Ala	Arg	Glu	Gly	Ala	Gln	Arg	Pro	Arg	Phe	Ile	Ser	705	710	715
Pro	Ala	Ser	Gln	Val	Ala	Ile	Cys	Leu	Ala	Leu	Ile	Ser	Gly	Gln	Leu	725	730	735
Leu	Ile	Val	Val	Ala	Trp	Leu	Val	Val	Glu	Ala	Pro	Gly	Thr	Gly	Lys	740	745	750
Glu	Thr	Ala	Pro	Glu	Arg	Arg	Glu	Val	Val	Thr	Leu	Arg	Cys	Asn	His	755	760	765
Arg	Asp	Ala	Ser	Met	Leu	Gly	Ser	Leu	Ala	Tyr	Asn	Val	Leu	Leu	Ile	770	775	780
Ala	Leu	Cys	Thr	Leu	Tyr	Ala	Phe	Asn	Thr	Arg	Lys	Cys	Pro	Glu	Asn	785	790	795
Phe	Asn	Glu	Ala	Lys	Phe	Ile	Gly	Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	805	810	815
Ile	Trp	Leu	Ala	Leu	Leu	Pro	Ile	Phe	Tyr	Val	Thr	Ser	Ser	Asp	Tyr	820	825	830
Arg	Val	Gln	Thr	Thr	Thr	Met	Cys	Val	Ser	Val	Ser	Leu	Ser	Gly	Ser	835	840	845
Val	Val	Leu	Gly	Cys	Leu	Phe	Ala	Pro	Lys	Leu	His	Ile	Ile	Leu	Phe	850	855	860
Gln	Pro	Gln	Lys	Asn	Val	Val	Ser	His	Arg	Ala	Pro	Thr	Ser	Arg	Phe	865	870	875
Gly	Ser	Ala	Ala	Ala	Arg	Ala	Ser	Ser	Ser	Leu	Gly	Gln	Gly	Ser	Gly			

				885					890					895	
Ser	Gln	Phe	Val	Pro	Thr	Val	Cys	Asn	Gly	Arg	Glu	Val	Val	Asp	Ser
			900					905						910	
Thr	Thr	Ser	Ser	Leu	Met	Thr	Leu	Glu	Ser	Ile	Met	Ala	Cys	Cys	Leu
		915					920					925			
Ser	Glu	Glu	Ala	Lys	Glu	Ala	Arg	Arg	Ile	Asn	Asp	Glu	Ile	Glu	Arg
	930					935					940				
Gln	Leu	Arg	Arg	Asp	Lys	Arg	Asp	Ala	Arg	Arg	Glu	Leu	Lys	Leu	Leu
945					950				955						960
Leu	Leu	Gly	Thr	Gly	Glu	Ser	Gly	Lys	Ser	Thr	Phe	Ile	Lys	Gln	Met
				965					970					975	
Arg	Ile	Ile	His	Gly	Ser	Gly	Tyr	Ser	Asp	Glu	Asp	Lys	Arg	Gly	Phe
			980					985					990		
Thr	Lys	Leu	Val	Tyr	Gln	Asn	Ile	Phe	Thr	Ala	Met	Gln	Ala	Met	Ile
	995						1000					1005			
Arg	Ala	Met	Asp	Thr	Leu	Lys	Ile	Pro	Tyr	Lys	Tyr	Glu	His	Asn	
	1010					1015					1020				
Lys	Ala	His	Ala	Gln	Leu	Val	Arg	Glu	Val	Asp	Val	Glu	Lys	Val	
	1025					1030					1035				
Ser	Ala	Phe	Glu	Asn	Pro	Tyr	Val	Asp	Ala	Ile	Lys	Ser	Leu	Trp	
	1040					1045					1050				
Asn	Asp	Pro	Gly	Ile	Gln	Glu	Cys	Tyr	Asp	Arg	Arg	Arg	Glu	Tyr	
	1055					1060					1065				
Gln	Leu	Ser	Asp	Ser	Thr	Lys	Tyr	Tyr	Leu	Asn	Asp	Leu	Asp	Arg	
	1070					1075					1080				
Val	Ala	Asp	Pro	Ala	Tyr	Leu	Pro	Thr	Gln	Gln	Asp	Val	Leu	Arg	
	1085					1090					1095				
Val	Arg	Val	Pro	Thr	Thr	Gly	Ile	Ile	Glu	Tyr	Pro	Phe	Asp	Leu	
	1100					1105					1110				
Gln	Ser	Val	Ile	Phe	Arg	Met	Val	Asp	Val	Gly	Gly	Gln	Arg	Ser	
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Glu	Arg	Arg	Lys	Trp	Ile	His	Cys	Phe	Glu	Asn	Val	Thr	Ser	Ile
1130						1135					1140			
Met	Phe	Leu	Val	Ala	Leu	Ser	Glu	Tyr	Asp	Gln	Val	Leu	Val	Glu
1145						1150					1155			
Ser	Asp	Asn	Glu	Asn	Arg	Met	Glu	Glu	Ser	Lys	Ala	Leu	Phe	Arg
1160						1165					1170			
Thr	Ile	Ile	Thr	Tyr	Pro	Trp	Phe	Gln	Asn	Ser	Ser	Val	Ile	Leu
1175						1180					1185			
Phe	Leu	Asn	Lys	Lys	Asp	Leu	Leu	Glu	Glu	Lys	Ile	Met	Tyr	Ser
1190						1195					1200			
His	Leu	Val	Asp	Tyr	Phe	Pro	Glu	Tyr	Asp	Gly	Pro	Gln	Arg	Asp
1205						1210					1215			
Ala	Gln	Ala	Ala	Arg	Glu	Phe	Ile	Leu	Lys	Met	Phe	Val	Asp	Leu
1220						1225					1230			
Asn	Pro	Asp	Ser	Asp	Lys	Ile	Ile	Tyr	Ser	His	Phe	Thr	Cys	Ala
1235						1240					1245			
Thr	Asp	Thr	Glu	Asn	Ile	Arg	Phe	Val	Phe	Ala	Ala	Val	Lys	Asp
1250						1255					1260			
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<210> 34

<211> 3105

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> chimeric hmGluR1/hCaR

<400> 34

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caccagaagg	gcggcccagc	agaggactgt	ggctcctgtca	atgagcaccg	tggcatccag	180

cgcttgagg	ccatgctttt	tgcactggac	cgcatcaacc	gtgaccgcga	cctgctgcct	240
ggcgtgcgc	tgggtgcaca	cactctcgac	agttgctcca	aggacacaca	tgcgctggag	300
caggcactgg	actttgtgcg	tgcctcactc	agccgtgggtg	ctgatggctc	acgccacatc	360
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ccacagatta	gctacgcctc	taccagtgcc	aagctgagtg	acaagtcccg	ctatgactac	540
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cccagtgcgc	gcgtggctgt	cctgttcacc	cgttctgagg	atgcccgga	gctgcttgct	840
gccagccagc	gcctcaatgc	cagcttcacc	tgggtggcca	gtgatgggtg	gggggcccctg	900
gagagtgtgg	tggcaggcag	tgagggggct	gctgaggggtg	ctatcaccat	cgagctggcc	960
tcctacccca	tcagtgaact	tgcctcctac	ttccagagcc	tggacccttg	gaacaacagc	1020
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cagcagcagc	ccctgaccct	cccacagcag	caacgatctc	agcagcagcc	cagatgcaag	2760
cagaagggtca	tctttggcag	cggcacggtc	accttctcac	tgagctttga	tgagcctcag	2820
aagaacgcca	tggcccacgg	gaattctacg	caccagaact	ccctggaggc	ccagaaaagc	2880
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gatctgaccg	tccaggaaac	aggtctgcaa	ggacctgtgg	gtggagacca	gcggccagag	3000

gtggaggacc ctgaagagtt gtccccagca cttgtagtgt ccagttcaca gagctttgtc 3060

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<210> 35

<211> 1035

<212> PRT

<213> Artificial Sequence

<220>

<221> misc_feature

<223> chimeric hmGluR1/hCaR

<400> 35

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Val Ala Glu Gly Pro Ala Lys Lys Val Leu Thr Leu Glu Gly Asp Leu
20 25 30

Val Leu Gly Gly Leu Phe Pro Val His Gln Lys Gly Gly Pro Ala Glu
35 40 45

Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala
50 55 60

Met Leu Phe Ala Leu Asp Arg Ile Asn Arg Asp Pro His Leu Leu Pro
65 70 75 80

Gly Val Arg Leu Gly Ala His Ile Leu Asp Ser Cys Ser Lys Asp Thr
85 90 95

His Ala Leu Glu Gln Ala Leu Asp Phe Val Arg Ala Ser Leu Ser Arg
100 105 110

Gly Ala Asp Gly Ser Arg His Ile Cys Pro Asp Gly Ser Tyr Ala Thr
115 120 125

His Gly Asp Ala Pro Thr Ala Ile Thr Gly Val Ile Gly Gly Ser Tyr
130 135 140

Ser Asp Val Ser Ile Gln Val Ala Asn Leu Leu Arg Leu Phe Gln Ile

145					150					155					160
Pro	Gln	Ile	Ser	Tyr	Ala	Ser	Thr	Ser	Ala	Lys	Leu	Ser	Asp	Lys	Ser
				165					170					175	
Arg	Tyr	Asp	Tyr	Phe	Ala	Arg	Thr	Val	Pro	Pro	Asp	Phe	Phe	Gln	Ala
			180					185						190	
Lys	Ala	Met	Ala	Glu	Ile	Leu	Arg	Phe	Phe	Asn	Trp	Thr	Tyr	Val	Ser
		195					200					205			
Thr	Val	Ala	Ser	Glu	Gly	Asp	Tyr	Gly	Glu	Thr	Gly	Ile	Glu	Ala	Phe
	210					215					220				
Glu	Leu	Glu	Ala	Arg	Ala	Arg	Asn	Ile	Cys	Val	Ala	Thr	Ser	Glu	Lys
225					230					235					240
Val	Gly	Arg	Ala	Met	Ser	Arg	Ala	Ala	Phe	Glu	Gly	Val	Val	Arg	Ala
				245					250					255	
Leu	Leu	Gln	Lys	Pro	Ser	Ala	Arg	Val	Ala	Val	Leu	Phe	Thr	Arg	Ser
			260					265					270		
Glu	Asp	Ala	Arg	Glu	Leu	Leu	Ala	Ala	Ser	Gln	Arg	Leu	Asn	Ala	Ser
		275					280					285			
Phe	Thr	Trp	Val	Ala	Ser	Asp	Gly	Trp	Gly	Ala	Leu	Glu	Ser	Val	Val
	290					295					300				
Ala	Gly	Ser	Glu	Gly	Ala	Ala	Glu	Gly	Ala	Ile	Thr	Ile	Glu	Leu	Ala
305					310					315					320
Ser	Tyr	Pro	Ile	Ser	Asp	Phe	Ala	Ser	Tyr	Phe	Gln	Ser	Leu	Asp	Pro
				325					330					335	
Trp	Asn	Asn	Ser	Arg	Asn	Pro	Trp	Phe	Arg	Glu	Phe	Trp	Glu	Gln	Arg
			340					345					350		
Phe	Arg	Cys	Ser	Phe	Arg	Gln	Arg	Asp	Cys	Ala	Ala	His	Ser	Leu	Arg
		355					360					365			
Ala	Val	Pro	Phe	Glu	Gln	Glu	Ser	Lys	Ile	Met	Phe	Val	Val	Asn	Ala
	370					375					380				
Val	Tyr	Ala	Met	Ala	His	Ala	Leu	His	Asn	Met	His	Arg	Ala	Leu	Cys
385					390					395					400

Pro	Asn	Thr	Thr	Arg	Leu	Cys	Asp	Ala	Met	Arg	Pro	Val	Asn	Gly	Arg	
				405					410					415		
Arg	Leu	Tyr	Lys	Asp	Phe	Val	Leu	Asn	Val	Lys	Phe	Asp	Ala	Pro	Phe	
			420					425					430			
Arg	Pro	Ala	Asp	Thr	His	Asn	Glu	Val	Arg	Phe	Asp	Arg	Phe	Gly	Asp	
		435					440					445				
Gly	Ile	Gly	Arg	Tyr	Asn	Ile	Phe	Thr	Tyr	Leu	Arg	Ala	Gly	Ser	Gly	
	450					455					460					
Arg	Tyr	Arg	Tyr	Gln	Lys	Val	Gly	Tyr	Trp	Ala	Glu	Gly	Leu	Thr	Leu	
465					470					475					480	
Asp	Thr	Ser	Leu	Ile	Pro	Trp	Ala	Ser	Pro	Ser	Ala	Gly	Pro	Leu	Pro	
				485					490					495		
Ala	Ser	Arg	Cys	Ser	Glu	Pro	Cys	Leu	Gln	Asn	Glu	Val	Lys	Ser	Val	
			500					505					510			
Gln	Pro	Gly	Glu	Val	Cys	Cys	Trp	Leu	Cys	Ile	Pro	Cys	Gln	Pro	Tyr	
		515					520					525				
Glu	Tyr	Arg	Leu	Asp	Glu	Phe	Thr	Cys	Ala	Asp	Cys	Gly	Leu	Gly	Tyr	
	530					535					540					
Trp	Pro	Asn	Ala	Ser	Leu	Thr	Gly	Cys	Phe	Glu	Leu	Pro	Gln	Glu	Tyr	
545					550					555					560	
Ile	Arg	Trp	Gly	Asp	Ala	Trp	Ala	Val	Gly	Pro	Val	Thr	Ile	Ala	Cys	
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Leu	Gly	Ala	Leu	Ala	Thr	Leu	Phe	Val	Leu	Gly	Val	Phe	Val	Arg	His	
			580					585					590			
Asn	Ala	Thr	Pro	Val	Val	Lys	Ala	Ser	Gly	Arg	Glu	Leu	Cys	Tyr	Ile	
		595					600					605				
Leu	Leu	Gly	Gly	Val	Phe	Leu	Cys	Tyr	Cys	Met	Thr	Phe	Ile	Phe	Ile	
	610					615					620					
Ala	Lys	Pro	Ser	Thr	Ala	Val	Cys	Thr	Leu	Arg	Arg	Leu	Gly	Leu	Gly	
625					630					635					640	
Thr	Ala	Phe	Ser	Val	Cys	Tyr	Ser	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg	
				645					650					655		

Ile	Ala	Arg	Ile	Phe	Gly	Gly	Ala	Arg	Glu	Gly	Ala	Gln	Arg	Pro	Arg
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Phe	Ile	Ser	Pro	Ala	Ser	Gln	Val	Ala	Ile	Cys	Leu	Ala	Leu	Ile	Ser
		675					680					685			
Gly	Gln	Leu	Leu	Ile	Val	Val	Ala	Trp	Leu	Val	Val	Glu	Ala	Pro	Gly
	690					695					700				
Thr	Gly	Lys	Glu	Thr	Ala	Pro	Glu	Arg	Arg	Glu	Val	Val	Thr	Leu	Arg
705					710					715					720
Cys	Asn	His	Arg	Asp	Ala	Ser	Met	Leu	Gly	Ser	Leu	Ala	Tyr	Asn	Val
				725					730					735	
Leu	Leu	Ile	Ala	Leu	Cys	Thr	Leu	Tyr	Ala	Phe	Lys	Thr	Arg	Lys	Cys
			740					745					750		
Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys	Phe	Ile	Gly	Phe	Thr	Met	Tyr	Thr
		755					760					765			
Thr	Cys	Ile	Ile	Trp	Leu	Ala	Phe	Leu	Pro	Ile	Phe	Tyr	Val	Thr	Ser
	770					775					780				
Ser	Asp	Tyr	Arg	Val	Gln	Thr	Thr	Thr	Met	Cys	Val	Ser	Val	Ser	Leu
785					790					795					800
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				805					810					815	
Ile	Leu	Phe	Gln	Pro	Gln	Lys	Asn	Thr	Ile	Glu	Glu	Val	Arg	Cys	Ser
			820					825					830		
Thr	Ala	Ala	His	Ala	Phe	Lys	Val	Ala	Ala	Arg	Ala	Thr	Leu	Arg	Arg
		835					840					845			
Ser	Asn	Val	Ser	Arg	Lys	Arg	Ser	Ser	Ser	Leu	Gly	Gly	Ser	Thr	Gly
	850					855					860				
Ser	Thr	Pro	Ser	Ser	Ser	Ile	Ser	Ser	Lys	Ser	Asn	Ser	Glu	Asp	Pro
865					870					875					880
Phe	Pro	Gln	Pro	Glu	Arg	Gln	Lys	Gln	Gln	Gln	Pro	Leu	Ala	Leu	Thr
				885					890					895	
Gln	Gln	Glu	Gln	Gln	Gln	Gln	Pro	Leu	Thr	Leu	Pro	Gln	Gln	Gln	Arg

900	905	910
Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly		
915	920	925
Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met		
930	935	940
Ala His Gly Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser		
945	950	955
Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly		
965	970	975
Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro		
980	985	990
Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser		
995	1000	1005
Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly		
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<210> 36
 <211> 4185
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> pmGluR2//CaR*G qi5 fusion construct

<400> 36

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 <223> pmGluR2//CaR*G qi5 fusion construct

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 <213> Artificial Sequence

 <220>
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 <223> chimeric hmGluR8/hCaR

 <400> 39

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Tyr	Ala	Ile	Asp	Gln	Ile	Asn	Lys	Asp	Pro	Asp	Leu	Leu	Ser	Asn	Ile
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Thr	Leu	Gly	Val	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr	Ala
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Ser	Asp	Val	Lys	Cys	Ala	Asn	Gly	Asp	Pro	Pro	Ile	Phe	Thr	Lys	Pro
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Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr
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Ser	Ile	Asp	Gly	Phe	Asp	Arg	Tyr	Phe	Arg	Ser	Arg	Thr	Leu	Ala	Asn	340		345	350
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Cys	Lys	Leu	Gly	Ser	His	Gly	Lys	Arg	Asn	Ser	His	Ile	Lys	Lys	Cys	370		375	380
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Val	Asn	Phe	Asn	Gly	Ser	Ala	Gly	Thr	Pro	Val	Thr	Phe	Asn	Glu	Asn	450	455	460	
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Lys	Ser	Thr	Glu	Tyr	Lys	Val	Ile	Gly	His	Trp	Thr	Asn	Gln	Leu	His		485	490	495
Leu	Lys	Val	Glu	Asp	Met	Gln	Trp	Ala	His	Arg	Glu	His	Thr	His	Pro	500		505	510
Ala	Ser	Val	Cys	Ser	Leu	Pro	Cys	Lys	Pro	Gly	Glu	Arg	Lys	Lys	Thr	515	520		525
Val	Lys	Gly	Val	Pro	Cys	Cys	Trp	His	Cys	Glu	Arg	Cys	Glu	Gly	Tyr	530	535	540	
Asn	Tyr	Gln	Val	Asp	Glu	Leu	Ser	Cys	Glu	Leu	Cys	Pro	Leu	Asp	Gln	545	550	555	560

Arg	Pro	Asn	Met	Asn	Arg	Thr	Gly	Cys	Gln	Leu	Ile	Pro	Ile	Ile	Lys	565	570	575
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Leu	Gly	Ile	Ile	Ala	Thr	Thr	Phe	Val	Ile	Val	Thr	Phe	Val	Arg	Tyr	595	600	605
Asn	Asp	Thr	Pro	Ile	Val	Arg	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	Val	610	615	620
Leu	Leu	Thr	Gly	Ile	Phe	Leu	Cys	Tyr	Ser	Ile	Thr	Phe	Leu	Met	Ile	625	630	635
Ala	Ala	Pro	Asp	Thr	Ile	Ile	Cys	Ser	Phe	Arg	Arg	Val	Phe	Leu	Gly	645	650	655
Leu	Gly	Met	Cys	Phe	Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg	660	665	670
Ile	His	Arg	Ile	Phe	Glu	Gln	Gly	Lys	Lys	Ser	Val	Thr	Ala	Pro	Lys	675	680	685
Phe	Ile	Ser	Pro	Ala	Ser	Gln	Leu	Val	Ile	Thr	Phe	Ser	Leu	Ile	Ser	690	695	700
Val	Gln	Leu	Leu	Gly	Val	Phe	Val	Trp	Phe	Val	Val	Asp	Pro	Pro	His	705	710	715
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Arg	Gly	Val	Leu	Lys	Cys	Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys	Ser	740	745	750
Leu	Gly	Tyr	Ser	Ile	Leu	Leu	Met	Val	Thr	Cys	Thr	Val	Tyr	Ala	Ile	755	760	765
Lys	Thr	Arg	Gly	Val	Pro	Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile	Gly	770	775	780
Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	Ile	Trp	Leu	Ala	Phe	Ile	Pro	Ile	785	790	795
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			980					985					990						
Pro	Leu	Leu	Pro	Leu	Gln	Cys	Gly	Glu	Thr	Asp	Leu	Asp	Leu	Thr	Val				
		995					1000					1005							
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	1010					1015					1020								
Glu	Val	Glu	Asp	Pro	Glu	Glu	Leu	Ser	Pro	Ala	Leu	Val	Val	Ser					
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<212> DNA
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Ser	Gln	Glu	Tyr	Ala	His	Ser	Ile	Arg	Val	Asp	Gly	Asp	Ile	Ile	Leu
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Tyr	Ala	Ile	Asp	Gln	Ile	Asn	Lys	Asp	Pro	Asp	Leu	Leu	Ser	Asn	Ile
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Thr	Leu	Gly	Val	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr	Ala
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		115					120					125			
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	130					135					140				
Asp	Lys	Ile	Ser	Gly	Val	Ile	Gly	Ala	Ala	Ala	Ser	Ser	Val	Ser	Ile
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Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr
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Ala	Ser	Thr	Ala	Pro	Glu	Leu	Ser	Asp	Asn	Thr	Arg	Tyr	Asp	Phe	Phe
			180					185					190		
Ser	Arg	Val	Val	Pro	Pro	Asp	Ser	Tyr	Gln	Ala	Gln	Ala	Met	Val	Asp
		195					200					205			
Ile	Val	Thr	Ala	Leu	Gly	Trp	Asn	Tyr	Val	Ser	Thr	Leu	Ala	Ser	Glu
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Gly	Asn	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Thr	Gln	Ile	Ser	Arg
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			260					265					270		
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Trp	Ile	Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Tyr	Gln	305	310	315			320
Gln	Glu	Glu	Ile	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Ala			330			335
Ser	Ile	Asp	Gly	Phe	Asp	Arg	Tyr	Phe	Arg	Ser	Arg	Thr	Leu	Ala	Asn		340	345			350
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Cys	Lys	Leu	Gly	Ser	His	Gly	Lys	Arg	Asn	Ser	His	Ile	Lys	Lys	Cys	370		375			380
Thr	Gly	Leu	Glu	Arg	Ile	Ala	Arg	Asp	Ser	Ser	Tyr	Glu	Gln	Glu	Gly	385		390			395
Lys	Val	Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ser	Met	Ala	Tyr	Ala	Leu		405	410			415
His	Asn	Met	His	Lys	Asp	Leu	Cys	Pro	Gly	Tyr	Ile	Gly	Leu	Cys	Pro		420	425			430
Arg	Met	Ser	Thr	Ile	Asp	Gly	Lys	Glu	Leu	Leu	Gly	Tyr	Ile	Arg	Ala		435	440			445
Val	Asn	Phe	Asn	Gly	Ser	Ala	Gly	Thr	Pro	Val	Thr	Phe	Asn	Glu	Asn	450		455			460
Gly	Asp	Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Phe	Gln	Tyr	Gln	Ile	Thr	Asn	465		470			475
Lys	Ser	Thr	Glu	Tyr	Lys	Val	Ile	Gly	His	Trp	Thr	Asn	Gln	Leu	His		485	490			495
Leu	Lys	Val	Glu	Asp	Met	Gln	Trp	Ala	His	Arg	Glu	His	Thr	His	Pro		500	505			510
Ala	Ser	Val	Cys	Ser	Leu	Pro	Cys	Lys	Pro	Gly	Glu	Arg	Lys	Lys	Thr		515	520			525
Val	Lys	Gly	Val	Pro	Cys	Cys	Trp	His	Cys	Glu	Arg	Cys	Glu	Gly	Tyr	530		535			540
Asn	Tyr	Gln	Val	Asp	Glu	Leu	Ser	Cys	Glu	Leu	Cys	Pro	Leu	Asp	Gln	545		550			555

Arg	Pro	Asn	Met	Asn	Arg	Thr	Gly	Cys	Gln	Leu	Ile	Pro	Ile	Ile	Lys	565	570	575
Leu	Glu	Trp	His	Ser	Pro	Trp	Ala	Val	Val	Pro	Val	Phe	Val	Ala	Ile	580	585	590
Leu	Gly	Ile	Ile	Ala	Thr	Thr	Phe	Val	Ile	Val	Thr	Phe	Val	Arg	Tyr	595	600	605
Asn	Asp	Thr	Pro	Ile	Val	Arg	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	Val	610	615	620
Leu	Leu	Thr	Gly	Ile	Phe	Leu	Cys	Tyr	Ser	Ile	Thr	Phe	Leu	Met	Ile	625	630	635
Ala	Ala	Pro	Asp	Thr	Ile	Ile	Cys	Ser	Phe	Arg	Arg	Val	Phe	Leu	Gly	645	650	655
Leu	Gly	Met	Cys	Phe	Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg	660	665	670
Ile	His	Arg	Ile	Phe	Glu	Gln	Gly	Lys	Lys	Ser	Val	Thr	Ala	Pro	Lys	675	680	685
Phe	Ile	Ser	Pro	Ala	Ser	Gln	Leu	Val	Ile	Thr	Phe	Ser	Leu	Ile	Ser	690	695	700
Val	Gln	Leu	Leu	Gly	Val	Phe	Val	Trp	Phe	Val	Val	Asp	Pro	Pro	His	705	710	715
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Arg	Gly	Val	Leu	Lys	Cys	Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys	Ser	740	745	750
Leu	Gly	Tyr	Ser	Ile	Leu	Leu	Met	Val	Thr	Cys	Thr	Val	Tyr	Ala	Ile	755	760	765
Lys	Thr	Arg	Gly	Val	Pro	Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile	Gly	770	775	780
Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	Ile	Trp	Leu	Ala	Phe	Ile	Pro	Ile	785	790	795
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Ser	Ser	Leu	Gly	Gly	Ser	Thr	Gly	Ser	Thr	Pro	Ser	Ser	Ser	Ile	Ser
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			900					905					910		
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	930						935					940			
Gln	Lys	Val	Ile	Phe	Gly	Ser	Gly	Thr	Val	Thr	Phe	Ser	Leu	Ser	Phe
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			980						985				990		
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	1040					1045					1050				

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1100						1105					1110			
Phe	Ile	Lys	Gln	Met	Arg	Ile	Ile	His	Gly	Ser	Gly	Tyr	Ser	Asp
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1130						1135					1140			
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1160						1165					1170			
Glu	Val	Asp	Val	Glu	Lys	Val	Ser	Ala	Phe	Glu	Asn	Pro	Tyr	Val
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Asp	Ala	Ile	Lys	Ser	Leu	Trp	Asn	Asp	Pro	Gly	Ile	Gln	Glu	Cys
1190						1195					1200			
Tyr	Asp	Arg	Arg	Arg	Glu	Tyr	Gln	Leu	Ser	Asp	Ser	Thr	Lys	Tyr
1205						1210					1215			
Tyr	Leu	Asn	Asp	Leu	Asp	Arg	Val	Ala	Asp	Pro	Ala	Tyr	Leu	Pro
1220						1225					1230			
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Tyr Asp Gln Val Leu Val Glu Ser Asp Asn Glu Asn Arg Met Glu
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 Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe
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 Gln Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu
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 Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe
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 <212> DNA
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 <223> GABA-R2*Gqo5 fusion construct

 <400> 42

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<212> PRT
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<220>
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<223> GABA-R2*Gqo5 fusion construct

<400> 43

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				20				25					30					
Leu	Pro	Leu	Ala	Pro	Gly	Ala	Trp	Gly	Trp	Ala	Arg	Gly	Ala	Pro	Arg			
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Pro	Pro	Pro	Ser	Ser	Pro	Pro	Leu	Ser	Ile	Met	Gly	Leu	Met	Pro	Leu			
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Thr	Lys	Glu	Val	Ala	Lys	Gly	Ser	Ile	Gly	Arg	Gly	Val	Leu	Pro	Ala			
65					70					75					80			
Val	Glu	Leu	Ala	Ile	Glu	Gln	Ile	Arg	Asn	Glu	Ser	Leu	Leu	Arg	Pro			
				85					90					95				
Tyr	Phe	Leu	Asp	Leu	Arg	Leu	Tyr	Asp	Thr	Glu	Cys	Asp	Asn	Ala	Lys			
			100					105					110					
Gly	Leu	Lys	Ala	Phe	Tyr	Asp	Ala	Ile	Lys	Tyr	Gly	Pro	Asn	His	Leu			
		115					120					125						
Met	Val	Phe	Gly	Gly	Val	Cys	Pro	Ser	Val	Thr	Ser	Ile	Ile	Ala	Glu			
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Ser	Leu	Gln	Gly	Trp	Asn	Leu	Val	Gln	Leu	Ser	Phe	Ala	Ala	Thr	Thr			
145					150					155					160			
Pro	Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Phe	Phe	Arg	Thr	Val			
				165					170					175				
Pro	Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu	Lys	Leu	Leu	Lys	His			
			180					185					190					
Tyr	Gln	Trp	Lys	Arg	Val	Gly	Thr	Leu	Thr	Gln	Asp	Val	Gln	Arg	Phe			
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Ser	Glu	Val	Arg	Asn	Asp	Leu	Thr	Gly	Val	Leu	Tyr	Gly	Glu	Asp	Ile			
		210				215					220							
Glu	Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp	Pro	Cys	Thr	Ser	Val			
225					230					235					240			
Lys	Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile	Leu	Gly	Gln	Phe	Asp			
				245					250					255				
Gln	Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala	Tyr	Glu	Glu	Asn	Met			

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		275					280					285					
Trp	Trp	Glu	Gln	Val	His	Thr	Glu	Ala	Asn	Ser	Ser	Arg	Cys	Leu	Arg		
	290						295					300					
Lys	Asn	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile	Gly	Val	Asp	Phe	Glu		
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Pro	Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser	Gly	Lys	Thr	Pro	Gln		
				325					330					335			
Gln	Tyr	Glu	Arg	Glu	Tyr	Asn	Asn	Lys	Arg	Ser	Gly	Val	Gly	Pro	Ser		
			340						345				350				
Lys	Phe	His	Gly	Tyr	Ala	Tyr	Asp	Gly	Ile	Trp	Val	Ile	Ala	Lys	Thr		
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Leu	Gln	Arg	Ala	Met	Glu	Thr	Leu	His	Ala	Ser	Ser	Arg	His	Gln	Arg		
	370						375					380					
Ile	Gln	Asp	Phe	Asn	Tyr	Thr	Asp	His	Thr	Leu	Gly	Arg	Ile	Ile	Leu		
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				405					410					415			
Phe	Arg	Asn	Gly	Glu	Arg	Met	Gly	Thr	Ile	Lys	Phe	Thr	Gln	Phe	Gln		
			420						425				430				
Asp	Ser	Arg	Glu	Val	Lys	Val	Gly	Glu	Tyr	Asn	Ala	Val	Ala	Asp	Thr		
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Leu	Glu	Ile	Ile	Asn	Asp	Thr	Ile	Arg	Phe	Gln	Gly	Ser	Glu	Pro	Pro		
	450						455				460						
Lys	Asp	Lys	Thr	Ile	Ile	Leu	Glu	Gln	Leu	Arg	Lys	Ile	Ser	Leu	Pro		
465					470					475					480		
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				485					490					495			
Ser	Ala	Phe	Leu	Phe	Phe	Asn	Ile	Lys	Asn	Arg	Asn	Gln	Lys	Leu	Ile		
			500					505					510				

Lys	Met	Ser	Ser	Pro	Tyr	Met	Asn	Asn	Leu	Ile	Ile	Leu	Gly	Gly	Met
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Ser	Glu	Lys	Thr	Phe	Glu	Thr	Leu	Cys	Thr	Val	Arg	Thr	Trp	Ile	Leu
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Thr	Val	Gly	Tyr	Thr	Thr	Ala	Phe	Gly	Ala	Met	Phe	Ala	Lys	Thr	Trp
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Arg	Val	His	Ala	Ile	Phe	Lys	Asn	Val	Lys	Met	Lys	Lys	Lys	Ile	Ile
			580					585					590		
Lys	Asp	Gln	Lys	Leu	Leu	Val	Ile	Val	Gly	Gly	Met	Leu	Leu	Ile	Asp
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		675					680					685			
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Phe	Cys	Ile	Val	Ala	Leu	Val	Ile	Ile	Phe	Cys	Ser	Thr	Ile	Thr	Leu
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Cys	Leu	Val	Phe	Val	Pro	Lys	Leu	Ile	Thr	Leu	Arg	Thr	Asn	Pro	Asp
			740					745					750		
Ala	Ala	Thr	Gln	Asn	Arg	Arg	Phe	Gln	Phe	Thr	Gln	Asn	Gln	Lys	Lys
		755					760					765			

Glu	Asp	Ser	Lys	Thr	Ser	Thr	Ser	Val	Thr	Ser	Val	Asn	Gln	Ala	Ser		
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Thr	Ser	Arg	Leu	Glu	Gly	Leu	Gln	Ser	Glu	Asn	His	Arg	Leu	Arg	Met		
	785				790					795					800		
Lys	Ile	Thr	Glu	Leu	Asp	Lys	Asp	Leu	Glu	Glu	Val	Thr	Met	Gln	Leu		
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Gln	Asp	Thr	Pro	Glu	Lys	Thr	Thr	Tyr	Ile	Lys	Gln	Asn	His	Tyr	Gln		
			820					825					830				
Glu	Leu	Asn	Asp	Ile	Leu	Asn	Leu	Gly	Asn	Phe	Thr	Glu	Ser	Thr	Asp		
		835					840					845					
Gly	Gly	Lys	Ala	Ile	Leu	Lys	Asn	His	Leu	Asp	Gln	Asn	Pro	Gln	Leu		
	850					855					860						
Gln	Trp	Asn	Thr	Thr	Glu	Pro	Ser	Arg	Thr	Cys	Lys	Asp	Pro	Ile	Glu		
	865				870					875					880		
Asp	Ile	Asn	Ser	Pro	Glu	His	Ile	Gln	Arg	Arg	Leu	Ser	Leu	Gln	Leu		
				885					890					895			
Pro	Ile	Leu	His	His	Ala	Tyr	Leu	Pro	Ser	Ile	Gly	Gly	Val	Asp	Ala		
			900					905					910				
Ser	Cys	Val	Ser	Pro	Cys	Val	Ser	Pro	Thr	Ala	Ser	Pro	Arg	His	Arg		
		915					920					925					
His	Val	Pro	Pro	Ser	Phe	Arg	Val	Met	Val	Ser	Gly	Leu	Ala	Ala	Ala		
	930					935					940						
Met	Thr	Leu	Glu	Ser	Ile	Met	Ala	Cys	Cys	Leu	Ser	Glu	Glu	Ala	Lys		
	945				950					955					960		
Glu	Ala	Arg	Arg	Ile	Asn	Asp	Glu	Ile	Glu	Arg	Gln	Leu	Arg	Arg	Asp		
				965					970					975			
Lys	Arg	Asp	Ala	Arg	Arg	Glu	Leu	Lys	Leu	Leu	Leu	Leu	Gly	Thr	Gly		
			980					985					990				
Glu	Ser	Gly	Lys	Ser	Thr	Phe	Ile	Lys	Gln	Met	Arg	Ile	Ile	His	Gly		
		995					1000					1005					
Ser	Gly	Tyr	Ser	Asp	Glu	Asp	Lys	Arg	Gly	Phe	Thr	Lys	Leu	Val			

1010		1015		1020
Tyr Gln Asn Ile Phe Thr	Ala Met Gln Ala Met	Ile Arg Ala Met		
1025	1030	1035		
Asp Thr Leu Lys Ile Pro	Tyr Lys Tyr Glu His	Asn Lys Ala His		
1040	1045	1050		
Ala Gln Leu Val Arg Glu	Val Asp Val Glu Lys	Val Ser Ala Phe		
1055	1060	1065		
Glu Asn Pro Tyr Val Asp	Ala Ile Lys Ser Leu	Trp Asn Asp Pro		
1070	1075	1080		
Gly Ile Gln Glu Cys Tyr	Asp Arg Arg Arg Glu	Tyr Gln Leu Ser		
1085	1090	1095		
Asp Ser Thr Lys Tyr Tyr	Leu Asn Asp Leu Asp	Arg Val Ala Asp		
1100	1105	1110		
Pro Ala Tyr Leu Pro Thr	Gln Gln Asp Val Leu	Arg Val Arg Val		
1115	1120	1125		
Pro Thr Thr Gly Ile Ile	Glu Tyr Pro Phe Asp	Leu Gln Ser Val		
1130	1135	1140		
Ile Phe Arg Met Val Asp	Val Gly Gly Gln Arg	Ser Glu Arg Arg		
1145	1150	1155		
Lys Trp Ile His Cys Phe	Glu Asn Val Thr Ser	Ile Met Phe Leu		
1160	1165	1170		
Val Ala Leu Ser Glu Tyr	Asp Gln Val Leu Val	Glu Ser Asp Asn		
1175	1180	1185		
Glu Asn Arg Met Glu Glu	Ser Lys Ala Leu Phe	Arg Thr Ile Ile		
1190	1195	1200		
Thr Tyr Pro Trp Phe Gln	Asn Ser Ser Val Ile	Leu Phe Leu Asn		
1205	1210	1215		
Lys Lys Asp Leu Leu Glu	Glu Lys Ile Met Tyr	Ser His Leu Val		
1220	1225	1230		
Asp Tyr Phe Pro Glu Tyr	Asp Gly Pro Gln Arg	Asp Ala Gln Ala		
1235	1240	1245		

Ala	Arg	Glu	Phe	Ile	Leu	Lys	Met	Phe	Val	Asp	Leu	Asn	Pro	Asp
1250						1255					1260			
Ser	Asp	Lys	Ile	Asn	Tyr	Ser	His	Phe	Thr	Cys	Ala	Thr	Asp	Thr
1265						1270					1275			
Glu	Asn	Ile	Arg	Phe	Val	Phe	Ala	Ala	Val	Lys	Asp	Thr	Ile	Leu
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1295						1300								

<210> 44
 <211> 3969
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 <221> misc_feature
 <223> GABA-BR1a*Gqo5 fusion construct

 <400> 44

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ggctggccag ggggccaggc ctgccagccc gcggtggaga tggcgtgga ggacgtgaat	600
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 ggtctgtac 3969

<210> 45
 <211> 1324
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <223> GABA-BR1a*Gqo5 fusion construct

 <220>
 <221> MOD_RES
 <222> (464)..(464)
 <223> Xaa is unknown or other

 <400> 45

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			20					25					30		
Ile	His	Pro	Pro	Trp	Glu	Gly	Gly	Ile	Arg	Tyr	Arg	Gly	Leu	Thr	Arg
		35					40					45			
Asp	Gln	Val	Lys	Ala	Ile	Asn	Phe	Leu	Pro	Val	Asp	Tyr	Glu	Ile	Glu
	50					55					60				

Tyr	Val	Cys	Arg	Gly	Glu	Arg	Glu	Val	Val	Gly	Pro	Lys	Val	Arg	Lys	65	70	75	80
Cys	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	Ser	Arg	Cys	85	90	95	
Val	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Thr	Leu	Glu	Asn	Gly	Lys	Val	100	105	110	
Phe	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	Arg	Val	Asp	115	120	125	
Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	Arg	Ser	Ile	130	135	140	
Cys	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	Gln	Val	Asn	145	150	155	160
Arg	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	Leu	Phe	165	170	175	
Pro	Met	Ser	Gly	Gly	Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	Pro	Ala	Val	180	185	190	
Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp	195	200	205	
Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln	210	215	220	
Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	Ile	Lys	Ile	225	230	235	240
Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala	245	250	255	
Ala	Arg	Met	Trp	Asn	Leu	Ile	Val	Leu	Ser	Tyr	Gly	Ser	Ser	Ser	Pro	260	265	270	
Ala	Leu	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	275	280	285	
Ser	Ala	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	290	295	300	
Gly	Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	305	310	315	320

Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
 325 330 335
 Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys
 340 345 350
 Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu
 355 360 365
 Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
 370 375 380
 Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp
 385 390 395 400
 Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr
 405 410 415
 Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro
 420 425 430
 Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu
 435 440 445
 Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Xaa
 450 455 460
 Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu
 465 470 475 480
 Ala Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu
 485 490 495
 Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg
 500 505 510
 Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe
 515 520 525
 Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln
 530 535 540
 Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp
 545 550 555 560
 Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala

				565					570					575			
Asp	Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu		
			580					585					590				
Phe	Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val		
		595					600					605					
Val	Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln		
	610					615					620						
Asn	Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu		
625					630					635					640		
Ala	Leu	Ala	Ala	Val	Phe	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	Gly		
				645					650					655			
Arg	Asn	Gln	Phe	Pro	Phe	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	Gly		
			660					665					670				
Leu	Gly	Phe	Ser	Leu	Gly	Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	Trp		
		675					680					685					
Val	His	Thr	Val	Phe	Thr	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	Lys		
	690					695					700						
Thr	Leu	Glu	Pro	Trp	Lys	Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val	Gly		
705					710					715					720		
Met	Asp	Val	Leu	Thr	Leu	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	His		
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Arg	Thr	Ile	Glu	Thr	Phe	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp		
			740					745					750				
Val	Ser	Ile	Leu	Pro	Gln	Leu	Glu	His	Cys	Ser	Ser	Arg	Lys	Met	Asn		
		755					760					765					
Thr	Trp	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu		
	770					775					780						
Gly	Ile	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile		
785					790					795					800		
Asn	Asp	His	Arg	Ala	Val	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu		
				805					810					815			

Cys	Leu	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	Asp	820	825	830
Ala	Ala	Phe	Ala	Phe	Ala	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr	Ile	835	840	845
Thr	Leu	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	Thr	Arg	850	855	860
Gly	Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr	Met	Lys	Thr	Gly	Ser	Ser	865	870	875
Thr	Asn	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	Glu	Asn	885	890	895
Arg	Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	Ser	Glu	900	905	910
Leu	Arg	His	Gln	Leu	Gln	Ser	Arg	Gln	Gln	Leu	Arg	Ser	Arg	Arg	His	915	920	925
Pro	Pro	Thr	Pro	Pro	Glu	Pro	Ser	Gly	Gly	Leu	Pro	Arg	Gly	Pro	Pro	930	935	940
Glu	Pro	Pro	Asp	Arg	Leu	Ser	Cys	Asp	Gly	Ser	Arg	Val	His	Leu	Leu	945	950	955
Tyr	Lys	Ala	Ala	Ala	Met	Thr	Leu	Glu	Ser	Ile	Met	Ala	Cys	Cys	Leu	965	970	975
Ser	Glu	Glu	Ala	Lys	Glu	Ala	Arg	Arg	Ile	Asn	Asp	Glu	Ile	Glu	Arg	980	985	990
Gln	Leu	Arg	Arg	Asp	Lys	Arg	Asp	Ala	Arg	Arg	Glu	Leu	Lys	Leu	Leu	995	1000	1005
Leu	Leu	Gly	Thr	Gly	Glu	Ser	Gly	Lys	Ser	Thr	Phe	Ile	Lys	Gln		1010	1015	1020
Met	Arg	Ile	Ile	His	Gly	Ser	Gly	Tyr	Ser	Asp	Glu	Asp	Lys	Arg		1025	1030	1035
Gly	Phe	Thr	Lys	Leu	Val	Tyr	Gln	Asn	Ile	Phe	Thr	Ala	Met	Gln		1040	1045	1050
Ala	Met	Ile	Arg	Ala	Met	Asp	Thr	Leu	Lys	Ile	Pro	Tyr	Lys	Tyr		1055	1060	1065

Glu	His	Asn	Lys	Ala	His	Ala	Gln	Leu	Val	Arg	Glu	Val	Asp	Val
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1085						1090					1095			
Ser	Leu	Trp	Asn	Asp	Pro	Gly	Ile	Gln	Glu	Cys	Tyr	Asp	Arg	Arg
1100						1105					1110			
Arg	Glu	Tyr	Gln	Leu	Ser	Asp	Ser	Thr	Lys	Tyr	Tyr	Leu	Asn	Asp
1115						1120					1125			
Leu	Asp	Arg	Val	Ala	Asp	Pro	Ala	Tyr	Leu	Pro	Thr	Gln	Gln	Asp
1130						1135					1140			
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1145						1150					1155			
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1160						1165					1170			
Gln	Arg	Ser	Glu	Arg	Arg	Lys	Trp	Ile	His	Cys	Phe	Glu	Asn	Val
1175						1180					1185			
Thr	Ser	Ile	Met	Phe	Leu	Val	Ala	Leu	Ser	Glu	Tyr	Asp	Gln	Val
1190						1195					1200			
Leu	Val	Glu	Ser	Asp	Asn	Glu	Asn	Arg	Met	Glu	Glu	Ser	Lys	Ala
1205						1210					1215			
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1220						1225					1230			
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1250						1255					1260			
Gln	Arg	Asp	Ala	Gln	Ala	Ala	Arg	Glu	Phe	Ile	Leu	Lys	Met	Phe
1265						1270					1275			
Val	Asp	Leu	Asn	Pro	Asp	Ser	Asp	Lys	Ile	Ile	Tyr	Ser	His	Phe
1280						1285					1290			
Thr	Cys	Ala	Thr	Asp	Thr	Glu	Asn	Ile	Arg	Phe	Val	Phe	Ala	Ala

1295		1300		1305										
Val	Lys	Asp	Thr	Ile	Leu	Gln	Leu	Asn	Leu	Lys	Gly	Cys	Gly	Leu
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Tyr

<210> 46
 <211> 4231
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <223> pmGluR2//CaR*G qi5+Ala linker fusion construct

 <400> 46

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Pro	Gln	Ile	Ser	Tyr	Ala	Ser	Thr	Ser	Ala	Lys	Leu	Ser	Asp	Lys	Ser	165	170	175	
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Thr	Val	Ala	Ser	Glu	Gly	Asp	Tyr	Gly	Glu	Thr	Gly	Ile	Glu	Ala	Phe	210	215	220	
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Val	Gly	Arg	Ala	Met	Ser	Arg	Ala	Ala	Phe	Glu	Gly	Val	Val	Arg	Ala	245	250	255	
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Glu	Asp	Ala	Arg	Glu	Leu	Leu	Ala	Ala	Ser	Gln	Arg	Leu	Asn	Ala	Ser	275	280	285	
Phe	Thr	Trp	Val	Ala	Ser	Asp	Gly	Trp	Gly	Ala	Leu	Glu	Ser	Val	Val	290	295	300	
Ala	Gly	Ser	Glu	Gly	Ala	Ala	Glu	Gly	Ala	Ile	Thr	Ile	Glu	Leu	Ala	305	310	315	320

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 Trp Asn Asn Ser Arg Asn Pro Trp Phe Arg Glu Phe Trp Glu Gln Arg
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 Phe Arg Cys Ser Phe Arg Gln Arg Asp Cys Ala Ala His Ser Leu Arg
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 Val Tyr Ala Met Ala His Ala Leu His Asn Met His Arg Ala Leu Cys
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 Asp Thr Ser Leu Ile Pro Trp Ala Ser Pro Ser Ala Gly Pro Leu Pro
 485 490 495
 Ala Ser Arg Cys Ser Glu Pro Cys Leu Gln Asn Glu Val Lys Ser Val
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 Gln Pro Gly Glu Val Cys Cys Trp Leu Cys Ile Pro Cys Gln Pro Tyr
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 Ile Arg Trp Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys

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Val	Val	Gly	Ile	Ala	Ala	Thr	Leu	Phe	Val	Val	Ile	Thr	Phe	Val	Arg	
		595					600					605				
Tyr	Asn	Asp	Thr	Pro	Ile	Val	Lys	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	
	610					615					620					
Val	Leu	Leu	Ala	Gly	Ile	Phe	Leu	Cys	Tyr	Ala	Thr	Thr	Phe	Leu	Met	
625					630					635					640	
Ile	Ala	Glu	Pro	Asp	Leu	Gly	Thr	Cys	Ser	Leu	Arg	Arg	Ile	Phe	Leu	
				645					650					655		
Gly	Leu	Gly	Met	Ser	Ile	Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn	
			660					665					670			
Arg	Ile	Tyr	Arg	Ile	Phe	Glu	Gln	Gly	Lys	Arg	Ser	Val	Ser	Ala	Pro	
		675					680					685				
Arg	Phe	Ile	Ser	Pro	Ala	Ser	Gln	Leu	Ala	Ile	Thr	Phe	Ser	Leu	Ile	
	690					695					700					
Ser	Leu	Gln	Leu	Leu	Gly	Ile	Cys	Val	Trp	Phe	Val	Val	Asp	Pro	Ser	
705					710					715					720	
His	Ser	Val	Val	Asp	Phe	Gln	Asp	Gln	Arg	Thr	Leu	Asp	Pro	Arg	Phe	
				725					730					735		
Ala	Arg	Gly	Val	Leu	Lys	Cys	Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys	
			740					745					750			
Leu	Leu	Gly	Tyr	Ser	Met	Leu	Leu	Met	Val	Thr	Cys	Thr	Val	Tyr	Ala	
		755					760					765				
Ile	Lys	Thr	Arg	Gly	Val	Pro	Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile	
	770					775					780					
Gly	Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	Val	Trp	Leu	Ala	Phe	Ile	Pro	
785					790					795					800	
Ile	Phe	Phe	Gly	Thr	Ser	Gln	Ser	Ala	Asp	Lys	Leu	Tyr	Ile	Gln	Thr	
				805					810					815		
Thr	Thr	Leu	Thr	Val	Ser	Val	Ser	Leu	Ser	Ala	Ser	Val	Ser	Leu	Gly	
			820					825					830			

Met Leu Tyr Met Pro Lys Val Tyr Ile Ile Leu Phe His Pro Glu Gln
835 840 845

Asn Val Pro Lys Arg Lys Arg Ser Leu Lys Ala Val Val Thr Ala Ala
850 855 860

Thr Met Ser Asn Lys Phe Thr Gln Lys Gly Asn Phe Arg Pro Asn Gly
865 870 875 880

Glu Ala Lys Ser Glu Leu Cys Glu Asn Leu Glu Ala Pro Ala Leu Ala
885 890 895

Thr Lys Gln Thr Tyr Val Thr Tyr Thr Asn His Ala Ile
900 905

<210> 49
<211> 1422
<212> PRT
<213> Artificial Sequence

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<223> phmGluR4//CaR*AAA*G-alpha qi5 fusion construct

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Leu Thr Ala Lys Phe Tyr Trp Ile Leu Thr Met Met Gln Arg Thr His
20 25 30

Ser Gln Glu Tyr Ala His Ser Ile Arg Ile Asp Gly Asp Ile Thr Leu
35 40 45

Gly Gly Leu Phe Pro Val His Gly Arg Gly Ser Glu Gly Lys Pro Cys
50 55 60

Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
65 70 75 80

Phe Ala Leu Asp Arg Ile Asn Asn Asp Pro Asp Leu Leu Pro Asn Ile
85 90 95

Thr	Leu	Gly	Ala	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	His	Ala	
			100					105					110			
Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Glu	Lys	Asp	Gly	
		115					120					125				
Thr	Glu	Val	Arg	Cys	Gly	Ser	Gly	Gly	Pro	Pro	Ile	Ile	Thr	Lys	Pro	
	130					135					140					
Glu	Arg	Val	Val	Gly	Val	Ile	Gly	Ala	Ser	Gly	Ser	Ser	Val	Ser	Ile	
145					150					155					160	
Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr	
			165						170					175		
Ala	Ser	Thr	Ala	Pro	Asp	Leu	Ser	Asp	Asn	Ser	Arg	Tyr	Asp	Phe	Phe	
			180					185					190			
Ser	Arg	Val	Val	Pro	Ser	Asp	Thr	Tyr	Gln	Ala	Gln	Ala	Met	Val	Asp	
		195					200					205				
Ile	Val	Arg	Ala	Leu	Lys	Trp	Asn	Tyr	Val	Ser	Thr	Val	Ala	Ser	Glu	
	210					215					220					
Gly	Ser	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Ile	Gln	Lys	Ser	Arg	
225					230					235					240	
Glu	Asp	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Val	Lys	Ile	Pro	Arg	Glu	
				245					250					255		
Pro	Lys	Ala	Gly	Glu	Phe	Asp	Lys	Ile	Ile	Arg	Arg	Leu	Leu	Glu	Thr	
			260					265					270			
Ser	Asn	Ala	Arg	Ala	Val	Ile	Ile	Phe	Ala	Asn	Glu	Asp	Asp	Ile	Arg	
		275					280					285				
Arg	Val	Leu	Glu	Ala	Ala	Arg	Arg	Ala	Asn	Gln	Thr	Gly	His	Phe	Phe	
	290					295					300					
Trp	Met	Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Leu	His	
305					310					315					320	
Leu	Glu	Glu	Val	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Met	
				325					330					335		
Ser	Val	Arg	Gly	Phe	Asp	Arg	Tyr	Phe	Ser	Ser	Arg	Thr	Leu	Asp	Asn	
			340					345					350			

Asn	Arg	Arg	Asn	Ile	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Asp	Asn	Phe	His			
		355					360					365						
Cys	Lys	Leu	Ser	Arg	His	Ala	Leu	Lys	Lys	Gly	Ser	His	Val	Lys	Lys			
	370					375					380							
Cys	Thr	Asn	Arg	Glu	Arg	Ile	Gly	Gln	Asp	Ser	Ala	Tyr	Glu	Gln	Glu			
385					390					395					400			
Gly	Lys	Val	Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ala	Met	Gly	His	Ala			
				405					410					415				
Leu	His	Ala	Met	His	Arg	Asp	Leu	Cys	Pro	Gly	Arg	Val	Gly	Leu	Cys			
			420					425					430					
Pro	Arg	Met	Asp	Pro	Val	Asp	Gly	Thr	Gln	Leu	Leu	Lys	Tyr	Ile	Arg			
		435					440					445						
Asn	Val	Asn	Phe	Ser	Gly	Ile	Ala	Gly	Asn	Pro	Val	Thr	Phe	Asn	Glu			
	450					455					460							
Asn	Gly	Asp	Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Tyr	Gln	Tyr	Gln	Leu	Arg			
465					470					475					480			
Asn	Asp	Ser	Ala	Glu	Tyr	Lys	Val	Ile	Gly	Ser	Trp	Thr	Asp	His	Leu			
				485					490					495				
His	Leu	Arg	Ile	Glu	Arg	Met	His	Trp	Pro	Gly	Ser	Gly	Gln	Gln	Leu			
			500					505					510					
Pro	Arg	Ser	Ile	Cys	Ser	Leu	Pro	Cys	Gln	Pro	Gly	Glu	Arg	Lys	Lys			
		515					520					525						
Thr	Val	Lys	Gly	Met	Pro	Cys	Cys	Trp	His	Cys	Glu	Pro	Cys	Thr	Gly			
	530					535					540							
Tyr	Gln	Tyr	Gln	Val	Asp	Arg	Tyr	Thr	Cys	Lys	Thr	Cys	Pro	Tyr	Asp			
545					550					555					560			
Met	Arg	Pro	Thr	Glu	Asn	Arg	Thr	Gly	Cys	Arg	Pro	Ile	Pro	Ile	Ile			
				565					570					575				
Lys	Leu	Glu	Trp	Gly	Ser	Pro	Trp	Ala	Val	Leu	Pro	Leu	Phe	Leu	Ala			
			580					585					590					
Val	Val	Gly	Ile	Ala	Ala	Thr	Leu	Phe	Val	Val	Ile	Thr	Phe	Val	Arg			

595					600					605					
Tyr	Asn	Asp	Thr	Pro	Ile	Val	Lys	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr
	610					615					620				
Val	Leu	Leu	Ala	Gly	Ile	Phe	Leu	Cys	Tyr	Ala	Thr	Thr	Phe	Leu	Met
625					630					635					640
Ile	Ala	Glu	Pro	Asp	Leu	Gly	Thr	Cys	Ser	Leu	Arg	Arg	Ile	Phe	Leu
				645					650					655	
Gly	Leu	Gly	Met	Ser	Ile	Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn
			660					665					670		
Arg	Ile	Tyr	Arg	Ile	Phe	Glu	Gln	Gly	Lys	Arg	Ser	Val	Ser	Ala	Pro
		675					680					685			
Arg	Phe	Ile	Ser	Pro	Ala	Ser	Gln	Leu	Ala	Ile	Thr	Phe	Ser	Leu	Ile
	690					695					700				
Ser	Leu	Gln	Leu	Leu	Gly	Ile	Cys	Val	Trp	Phe	Val	Val	Asp	Pro	Ser
705					710					715					720
His	Ser	Val	Val	Asp	Phe	Gln	Asp	Gln	Arg	Thr	Leu	Asp	Pro	Arg	Phe
				725					730					735	
Ala	Arg	Gly	Val	Leu	Lys	Cys	Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys
			740					745					750		
Leu	Leu	Gly	Tyr	Ser	Met	Leu	Leu	Met	Val	Thr	Cys	Thr	Val	Tyr	Ala
		755					760					765			
Ile	Lys	Thr	Arg	Gly	Val	Pro	Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile
	770					775					780				
Gly	Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	Val	Trp	Leu	Ala	Phe	Ile	Pro
785					790					795					800
Ile	Phe	Phe	Gly	Thr	Ser	Gln	Ser	Ala	Asp	Lys	Leu	Tyr	Ile	Gln	Thr
				805					810					815	
Thr	Thr	Leu	Thr	Val	Ser	Val	Ser	Leu	Ser	Ala	Ser	Val	Ser	Leu	Gly
			820					825					830		
Met	Leu	Tyr	Met	Pro	Lys	Val	Tyr	Ile	Ile	Leu	Phe	His	Pro	Glu	Gln
		835					840					845			

Asn	Thr	Ile	Glu	Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	850	855	860	
Val	Ala	Ala	Arg	Ala	Thr	Leu	Arg	Arg	Ser	Asn	Val	Ser	Arg	Lys	Arg	865	870	875	880
Ser	Ser	Ser	Leu	Gly	Gly	Ser	Thr	Gly	Ser	Thr	Pro	Ser	Ser	Ser	Ile	885	890	895	
Ser	Ser	Lys	Ser	Asn	Ser	Glu	Asp	Pro	Phe	Pro	Gln	Pro	Glu	Arg	Gln	900	905	910	
Lys	Gln	Gln	Gln	Pro	Leu	Ala	Leu	Thr	Gln	Gln	Glu	Gln	Gln	Gln	Gln	915	920	925	
Pro	Leu	Thr	Leu	Pro	Gln	Gln	Gln	Arg	Ser	Gln	Gln	Gln	Pro	Arg	Cys	930	935	940	
Lys	Gln	Lys	Val	Ile	Phe	Gly	Ser	Gly	Thr	Val	Thr	Phe	Ser	Leu	Ser	945	950	955	960
Phe	Asp	Glu	Pro	Gln	Lys	Asn	Ala	Met	Ala	His	Gly	Asn	Ser	Thr	His	965	970	975	
Gln	Asn	Ser	Leu	Glu	Ala	Gln	Lys	Ser	Ser	Asp	Thr	Leu	Thr	Arg	His	980	985	990	
Gln	Pro	Leu	Leu	Pro	Leu	Gln	Cys	Gly	Glu	Thr	Asp	Leu	Asp	Leu	Thr	995	1000	1005	
Val	Gln	Glu	Thr	Gly	Leu	Gln	Gly	Pro	Val	Gly	Gly	Asp	Gln	Arg	1010	1015	1020		
Pro	Glu	Val	Glu	Asp	Pro	Glu	Glu	Leu	Ser	Pro	Ala	Leu	Val	Val	1025	1030	1035		
Ser	Ser	Ser	Gln	Ser	Phe	Val	Ile	Ser	Gly	Gly	Gly	Ser	Thr	Val	1040	1045	1050		
Thr	Glu	Asn	Val	Val	Asn	Ser	Ala	Ala	Ala	Met	Thr	Leu	Glu	Ser	1055	1060	1065		
Ile	Met	Ala	Cys	Cys	Leu	Ser	Glu	Glu	Ala	Lys	Glu	Ala	Arg	Arg	1070	1075	1080		
Ile	Asn	Asp	Glu	Ile	Glu	Arg	Gln	Leu	Arg	Arg	Asp	Lys	Arg	Asp	1085	1090	1095		

Ala	Arg	Arg	Glu	Leu	Lys	Leu	Leu	Leu	Gly	Thr	Gly	Glu	Ser	
1100						1105				1110				
Gly	Lys	Ser	Thr	Phe	Ile	Lys	Gln	Met	Arg	Ile	Ile	His	Gly	Ser
1115						1120					1125			
Gly	Tyr	Ser	Asp	Glu	Asp	Lys	Arg	Gly	Phe	Thr	Lys	Leu	Val	Tyr
1130						1135					1140			
Gln	Asn	Ile	Phe	Thr	Ala	Met	Gln	Ala	Met	Ile	Arg	Ala	Met	Asp
1145						1150					1155			
Thr	Leu	Lys	Ile	Pro	Tyr	Lys	Tyr	Glu	His	Asn	Lys	Ala	His	Ala
1160						1165					1170			
Gln	Leu	Val	Arg	Glu	Val	Asp	Val	Glu	Lys	Val	Ser	Ala	Phe	Glu
1175						1180					1185			
Asn	Pro	Tyr	Val	Asp	Ala	Ile	Lys	Ser	Leu	Trp	Asn	Asp	Pro	Gly
1190						1195					1200			
Ile	Gln	Glu	Cys	Tyr	Asp	Arg	Arg	Arg	Glu	Tyr	Gln	Leu	Ser	Asp
1205						1210					1215			
Ser	Thr	Lys	Tyr	Tyr	Leu	Asn	Asp	Leu	Asp	Arg	Val	Ala	Asp	Pro
1220						1225					1230			
Ala	Tyr	Leu	Pro	Thr	Gln	Gln	Asp	Val	Leu	Arg	Val	Arg	Val	Pro
1235						1240					1245			
Thr	Thr	Gly	Ile	Ile	Glu	Tyr	Pro	Phe	Asp	Leu	Gln	Ser	Val	Ile
1250						1255					1260			
Phe	Arg	Met	Val	Asp	Val	Gly	Gly	Gln	Arg	Ser	Glu	Arg	Arg	Lys
1265						1270					1275			
Trp	Ile	His	Cys	Phe	Glu	Asn	Val	Thr	Ser	Ile	Met	Phe	Leu	Val
1280						1285					1290			
Ala	Leu	Ser	Glu	Tyr	Asp	Gln	Val	Leu	Val	Glu	Ser	Asp	Asn	Glu
1295						1300					1305			
Asn	Arg	Met	Glu	Glu	Ser	Lys	Ala	Leu	Phe	Arg	Thr	Ile	Ile	Thr
1310						1315					1320			
Tyr	Pro	Trp	Phe	Gln	Asn	Ser	Ser	Val	Ile	Leu	Phe	Leu	Asn	Lys

1325		1330		1335
Lys Asp Leu Leu Glu Glu	Lys Ile Met Tyr Ser	His Leu Val Asp		
1340	1345	1350		
Tyr Phe Pro Glu Tyr Asp	Gly Pro Gln Arg Asp	Ala Gln Ala Ala		
1355	1360	1365		
Arg Glu Phe Ile Leu Lys	Met Phe Val Asp Leu	Asn Pro Asp Ser		
1370	1375	1380		
Asp Lys Ile Ile Tyr Ser	His Phe Thr Cys Ala	Thr Asp Thr Glu		
1385	1390	1395		
Asn Ile Arg Phe Val Phe	Ala Ala Val Lys Asp	Thr Ile Leu Gln		
1400	1405	1410		
Leu Asn Leu Lys Asp Cys	Gly Leu Phe			
1415	1420			

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 <223> Xaa is unknown or other

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Ser Gln Glu Tyr Ala His Ser Ile Arg Val Asp Gly Asp Ile Ile Leu		
35	40	45

Gly	Gly	Leu	Phe	Pro	Val	His	Ala	Lys	Gly	Glu	Arg	Gly	Val	Pro	Cys	
50						55					60					
Gly	Glu	Leu	Lys	Lys	Glu	Lys	Gly	Ile	His	Arg	Leu	Glu	Ala	Met	Leu	
65					70					75					80	
Tyr	Ala	Ile	Asp	Gln	Ile	Asn	Lys	Asp	Pro	Asp	Leu	Leu	Ser	Asn	Ile	
				85					90					95		
Thr	Leu	Gly	Val	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr	Ala	
			100					105					110			
Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Glu	Lys	Asp	Ala	
		115					120					125				
Ser	Asp	Val	Lys	Cys	Ala	Asn	Gly	Asp	Pro	Pro	Ile	Phe	Thr	Lys	Pro	
	130					135					140					
Asp	Lys	Ile	Ser	Gly	Val	Ile	Gly	Ala	Ala	Ala	Ser	Ser	Val	Ser	Ile	
145					150					155					160	
Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr	
				165					170					175		
Ala	Ser	Thr	Ala	Pro	Glu	Leu	Ser	Asp	Asn	Thr	Arg	Tyr	Asp	Phe	Phe	
			180					185					190			
Ser	Arg	Val	Val	Pro	Pro	Asp	Ser	Tyr	Gln	Ala	Gln	Ala	Met	Val	Asp	
		195					200					205				
Ile	Val	Thr	Ala	Leu	Gly	Trp	Asn	Tyr	Val	Ser	Thr	Leu	Ala	Ser	Glu	
	210					215					220					
Gly	Asn	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Thr	Gln	Ile	Ser	Arg	
225					230					235					240	
Glu	Ile	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Gln	Lys	Ile	Pro	Arg	Glu	
				245					250					255		
Pro	Arg	Pro	Gly	Glu	Phe	Glu	Lys	Ile	Ile	Lys	Arg	Leu	Leu	Glu	Thr	
			260					265					270			
Pro	Asn	Ala	Arg	Ala	Val	Ile	Met	Phe	Ala	Asn	Glu	Asp	Asp	Ile	Arg	
		275					280					285				
Arg	Ile	Leu	Glu	Ala	Ala	Lys	Lys	Leu	Asn	Gln	Ser	Gly	His	Phe	Leu	
	290					295					300					

Trp	Ile	Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Tyr	Gln	305	310	315	320
Gln	Glu	Glu	Ile	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Ala		325	330	335
Ser	Ile	Asp	Gly	Phe	Asp	Arg	Tyr	Phe	Arg	Ser	Arg	Thr	Leu	Ala	Asn	340		345	350
Asn	Arg	Arg	Asn	Val	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Glu	Asn	Phe	Gly	355		360	365
Cys	Lys	Leu	Gly	Ser	His	Gly	Lys	Arg	Asn	Xaa	Ser	His	Ile	Lys	Lys	370		375	380
Cys	Thr	Gly	Leu	Glu	Arg	Ile	Ala	Arg	Asp	Ser	Ser	Tyr	Glu	Gln	Glu	385		390	395
Gly	Lys	Val	Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ser	Met	Ala	Tyr	Ala		405	410	415
Leu	His	Asn	Met	His	Lys	Asp	Leu	Cys	Pro	Gly	Tyr	Ile	Gly	Leu	Cys		420	425	430
Pro	Arg	Met	Ser	Thr	Ile	Asp	Gly	Lys	Glu	Leu	Leu	Gly	Tyr	Ile	Arg	435		440	445
Ala	Val	Asn	Phe	Asn	Gly	Ser	Ala	Gly	Thr	Pro	Val	Thr	Phe	Asn	Glu	450		455	460
Asn	Gly	Asp	Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Phe	Gln	Tyr	Gln	Ile	Thr	465		470	475
Asn	Lys	Ser	Thr	Glu	Tyr	Lys	Val	Ile	Gly	His	Trp	Thr	Asn	Gln	Leu		485	490	495
His	Leu	Lys	Val	Glu	Asp	Met	Gln	Trp	Ala	His	Arg	Glu	His	Thr	His		500	505	510
Pro	Ala	Ser	Val	Cys	Ser	Leu	Pro	Cys	Lys	Pro	Gly	Glu	Arg	Lys	Lys	515		520	525
Thr	Val	Lys	Gly	Val	Pro	Cys	Cys	Trp	His	Cys	Glu	Arg	Cys	Glu	Gly	530		535	540
Tyr	Asn	Tyr	Gln	Val	Asp	Glu	Leu	Ser	Cys	Glu	Leu	Cys	Pro	Leu	Asp				

545					550					555					560
Gln	Arg	Pro	Asn	Met	Asn	Arg	Thr	Gly	Cys	Gln	Leu	Ile	Pro	Ile	Ile
				565					570					575	
Lys	Leu	Glu	Trp	His	Ser	Pro	Trp	Ala	Val	Val	Pro	Val	Phe	Val	Ala
			580					585					590		
Ile	Leu	Gly	Ile	Ile	Ala	Thr	Thr	Phe	Val	Ile	Val	Thr	Phe	Val	Arg
		595					600					605			
Tyr	Asn	Asp	Thr	Pro	Ile	Val	Arg	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr
	610					615					620				
Val	Leu	Leu	Thr	Gly	Ile	Phe	Leu	Cys	Tyr	Ser	Ile	Thr	Phe	Leu	Met
625					630					635					640
Ile	Ala	Ala	Pro	Asp	Thr	Ile	Ile	Cys	Ser	Phe	Arg	Arg	Val	Phe	Leu
				645					650					655	
Gly	Leu	Gly	Met	Cys	Phe	Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn
			660					665					670		
Arg	Ile	His	Arg	Ile	Phe	Glu	Gln	Gly	Lys	Lys	Ser	Val	Thr	Ala	Pro
		675					680					685			
Lys	Phe	Ile	Ser	Pro	Ala	Ser	Gln	Leu	Val	Ile	Thr	Phe	Ser	Leu	Ile
	690					695					700				
Ser	Val	Gln	Leu	Leu	Gly	Val	Phe	Val	Trp	Phe	Val	Val	Asp	Pro	Pro
705					710					715					720
His	Ile	Ile	Ile	Asp	Tyr	Gly	Glu	Gln	Arg	Thr	Leu	Asp	Pro	Glu	Lys
				725					730					735	
Ala	Arg	Gly	Val	Leu	Lys	Cys	Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys
			740					745					750		
Ser	Leu	Gly	Tyr	Ser	Ile	Leu	Leu	Met	Val	Thr	Cys	Thr	Val	Tyr	Ala
		755					760					765			
Ile	Lys	Thr	Arg	Gly	Val	Pro	Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile
	770					775					780				
Gly	Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	Ile	Trp	Leu	Ala	Phe	Ile	Pro
785					790					795					800

Ile	Phe	Phe	Gly	Thr	Ala	Gln	Ser	Ala	Glu	Lys	Met	Tyr	Ile	Gln	Thr	
				805					810					815		
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Arg Glu Phe Ile Leu Lys	Met Phe Val Asp Leu	Asn Pro Asp Ser		
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Asp Lys Ile Ile Tyr Ser	His Phe Thr Cys Ala	Thr Asp Thr Glu		
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